

91549

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From: Gibbs, Terra  
Sent: Tuesday, April 15, 2003 10:47 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request...

RECEIVED  
APR 15 2003  
(STIC)

Could you please do a regular search of SEQ ID NO:78 of USSN 09800629?

Please no EST's.

Terra Gibbs #79523  
AU 1635  
Mailbox 11E12  
306-3221

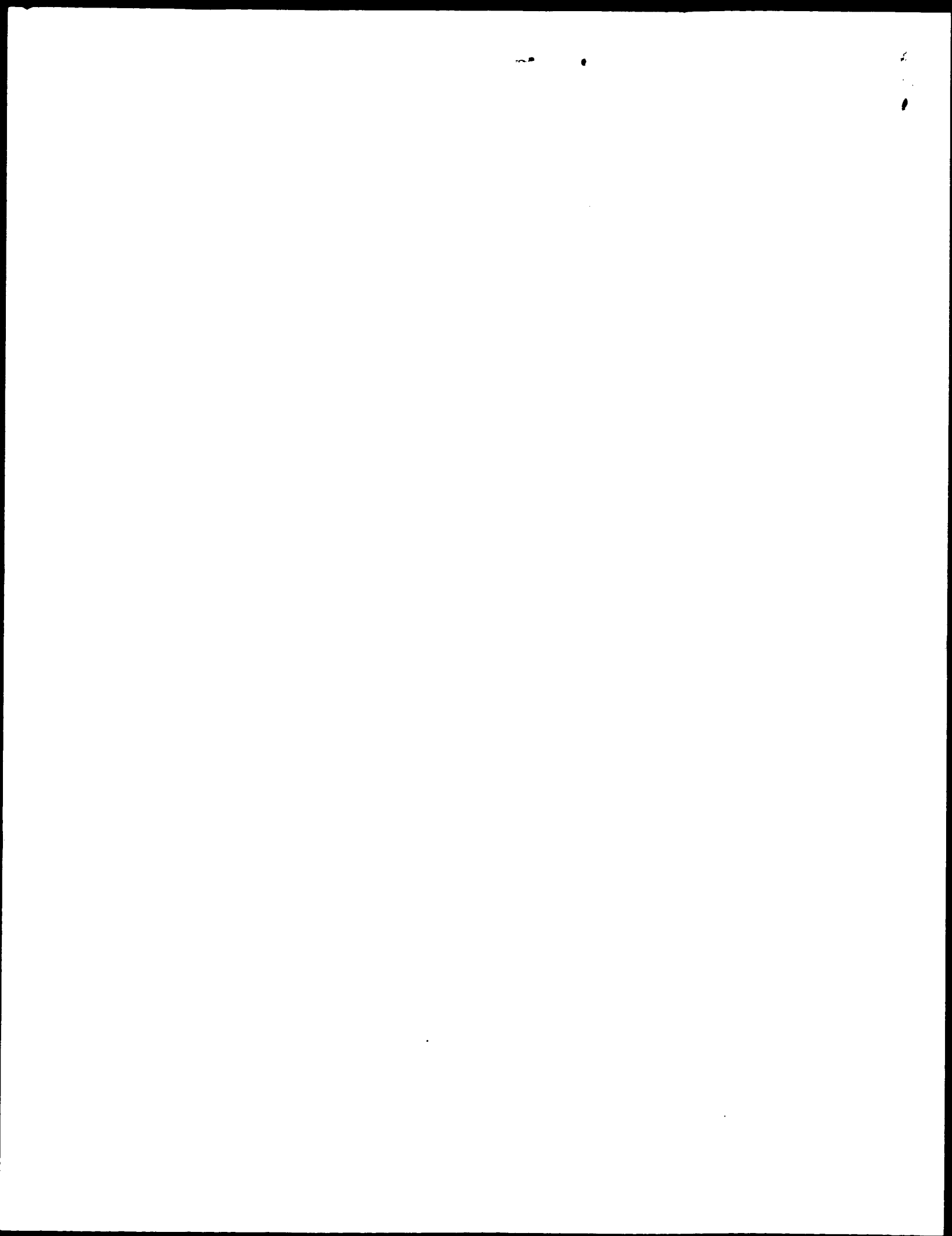
THANK YOU!

POINT OF CONTACT:  
PAUL SCHULWITZ  
TECHNICAL INFO. SPECIALIST  
CM1 6B06 TEL. (703) 305-1954

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 4/16  
Date Completed: 4/24  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 22:52:02 ; Search time 9284 Seconds

(without alignments)  
10125.168 Million cell updates/sec

Title: US-09-800-629A-78

Perfect score: 3230  
Sequence: 1 atcctatcaagaccaccagt.....aaactctctcaagatcc 3230

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :
1: gb_ba:*
2: gb_hhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: em_ba:*
16: em_fun:*
17: em_hhg:*
18: em_in:*
19: em_mu:*
20: em_om:*
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24: em_ph:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_hhg_hum:*
31: em_hhg_inv:*
32: em_hhg_other:*
33: em_hhg_mus:*
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35: em_hhg_rnd:*
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37: em_hhg_vrt:*
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39: em_hhg_hum:*
40: em_hhg_mus:*
41: em_hhg_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3230	100.0	3230	6 ARI36275	ARI36275 Sequence
2	3230	100.0	3230	6 E01640	E01640 gene for hu
3	3230	100.0	3230	9 HSBCEIFPI	X12706 H.sapiens g
4	3230	100.0	3230	9 HUMT15	J03478 Human Inter
5	3228.4	100.0	3230	6 E13592	E13592 gDNA encodi
6	2940	91.0	3241	9 HUMT15A	J02971 Human eosin
7	2940	91.0	5186	9 AF353265	AF353265 Homo sapi
8	2940	91.0	57186	9 AC004042	AC004042 Homo sapi
9	2940	91.0	160042	9 AC079320	AC079320 Homo sapi
10	2940	91.0	169385	9 AC116366	AC116366 Homo sapi
11	2256.2	69.9	3507	9 HUM21DC94Z	L48478 Homo sapien
12	1171.2	36.3	1395	6 A21910	A21910 partial gen
13	782.8	24.2	3710	9 HUM21DC93Z	L48477 Homo sapien
14	687	21.3	700	6 AX182853	AX182853 Sequence
15	686.4	21.3	700	6 AX182850	AX182850 Sequence
16	640.4	19.8	700	6 AX182852	AX182852 Sequence
17	627.4	19.4	700	6 AX182851	AX182851 Sequence
18	626	19.4	5397	6 AX345947	AX345947 Sequence
19	622.4	19.3	700	6 AX182854	AX182854 Sequence
20	616.4	19.1	5397	6 AX345946	AX345946 Sequence
21	600.6	18.6	1658	4 AF331920	AF331920 Canis fam
22	562.8	17.4	1140	4 OAI1V1	U17052 Ovis aries
23	479.4	14.8	816	6 E01639	E01639 CDNA encodi
24	479.4	14.8	816	6 E13591	E13591 CDNA encodi
25	479.4	14.8	816	9 HSBCEIFPI	X04688 Human mRNA
26	477.8	14.8	816	9 HSBCEIFPI	X12705 H.sapiens m
27	406.8	12.6	700	6 AX182849	AX182849 Sequence
28	367	11.4	367	11 G06365	G06365 human STS
29	360	11.1	1328	6 A87003	A87003 Sequence 94
30	360	11.1	1328	6 AR048415	AR048415 Sequence
31	354.4	11.0	700	6 AX182855	AX182855 Sequence
32	240.4	7.4	450	4 OAI1V2	U17053 Ovis aries
33	230.4	7.1	838	4 AF025436	AF025436 Felis cat
34	198.6	6.1	1945	10 RPTM5G	X54419 R.rattus ge
35	163.6	5.0	444	6 AX040771	AX040771 Sequence
36	161.8	5.0	6727	6 ARI36198	ARI36198 Sequence
37	161.8	5.0	6727	10 MM115G	X06271 Murine gene
38	161.8	5.0	121121	10 AL645741	AL645741 Mouse DNA
39	161.8	5.0	142732	10 AC084392	AC084392 Mus muscu
40	152.4	4.7	610	4 AF331919	AF331919 Canis fam
41	151.4	4.7	208236	2 AC073292	AC073292 Mus muscu
42	151.4	4.7	237823	2 AC020886	AC020886 Mus muscu
43	142.4	4.4	405	9 MMU19848	U19848 Macaca mula
44	136.2	4.2	405	9 CEY1N5A	L26033 Cercopithec
45	134.4	4.2	421	12 SYN1L5A	M33949 Synthetic h

#### ALIGNMENTS

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RESULT 1
LOCUS ARI36275 ARI36275 3230 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 78 from patent US 6136603.
ACCESSION ARI36275
VERSION ARI36275.1 GI:14476947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3230)
AUTHORS Dean,N.M., Kairas,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 78 24-OCT-2000;
FEATURES Location/Qualifiers
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source 1..3230 /organism="unknown"  
 BASE COUNT 1027 a 545 c 622 g 1036 t  
 ORIGIN  
 Query Match 100.0%; Score 3230; DB 6; Length 3230;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCATCAAGACCCAGTGAACAGACCTGACCCGCAAGCGTTGGATTTCATTT 60  
 Db 1 ATCCATCAAGACCCAGTGAACAGACCTGACCCGCAAGCGTTGGATTTCATTT 60  
 QY 61 CAATCACTGCTCCGCCAGCAGATTTTCAATTTCTTTAAGACAGATTATCAGCCACA 120  
 Db 61 CAATCACTGCTCCGCCAGCAGATTTTCAATTTCTTTAAGACAGATTATCAGCCACA 120  
 QY 121 GTCATAGTACAGATGCGCATCTTGAAAAAACAATTTCCCAATTTATGTAATTTAGC 180  
 Db 121 GTCATAGTACAGATGCGCATCTTGAAAAAACAATTTCCCAATTTATGTAATTTAGC 180  
 QY 181 ATAAATCTGTAGTGTCTACCTTATCTTTGTTTSCACACATCTTTAAGAGGAA 240  
 Db 181 ATAAATCTGTAGTGTCTACCTTATCTTTGTTTSCACACATCTTTAAGAGGAA 240  
 QY 241 GTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGTATTAACCCAAAGATT 300  
 Db 241 GTTAATTTCTGATTTTAAAGAAATGCAATGTGGGCAATGATGTATTAACCCAAAGATT 300  
 QY 301 CCTTCCGTATACAAAAATGTTTTAAAGGGGGAACAGGGATTTTATTTAAAAAGAT 360  
 Db 301 CCTTCCGTATACAAAAATGTTTTAAAGGGGGAACAGGGATTTTATTTAAAAAGAT 360  
 QY 361 AAAAGTAATTTATTTTAAAGATTAAGCATTAAGCAATTTAGTTTACAGATATGCC 420  
 Db 361 AAAAGTAATTTATTTTAAAGATTAAGCATTAAGCAATTTAGTTTACAGATATGCC 420  
 QY 421 ATTATTAAGCATTTCTATCTGATTTGTTAGAAATATATCTTTCCCAAGACAGCAAT 480  
 Db 421 ATTATTAAGCATTTCTATCTGATTTGTTAGAAATATATCTTTCCCAAGACAGCAAT 480  
 QY 481 AAATGTGCGGGAGAGCTGTACTATGACCTTTGTCGAAGGCAAGGAGAGAA 540  
 Db 481 AAATGTGCGGGAGAGCTGTACTATGACCTTTGTCGAAGGCAAGGAGAGAA 540  
 QY 541 CGTTTACAGACCATGAGGATGCTTGCATTTGAGTTTGTAGCTCTTGAGAGCTGCCAC 600  
 Db 541 CGTTTACAGACCATGAGGATGCTTGCATTTGAGTTTGTAGCTCTTGAGAGCTGCCAC 600  
 QY 601 GTGTATGCCATCCCCACAGAAATTTCCACAGATGATGTGTAAGAGACCTTGACACTG 660  
 Db 601 GTGTATGCCATCCCCACAGAAATTTCCACAGATGATGTGTAAGAGACCTTGAGACTG 660  
 QY 661 CTTTCTACTCATGCACTGCTGATAGCCAAATGAGTAATTTCTTTATGATTTCTTACA 720  
 Db 661 CTTTCTACTCATGCACTGCTGATAGCCAAATGAGTAATTTCTTTATGATTTCTTACA 720  
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 Db 721 GTCGTAAAGTGAAGTAATCATTTGATGAGTTCTTTACTATATATAGAGATCTGT 780  
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 Db 781 TATTAATTAATTAAGATTTGACATTTAGTACATTTGATGATTTGATTTGATTTGAT 840  
 QY 841 ATTCTGTTAAAGTATGATGCTGTGCTGCTTAAATAATGATTTGATTTGCTTTCTCT 900  
 Db 841 ATTCTGTTAAAGTATGATGCTGTGCTGCTTAAATAATGATTTGATTTGCTTTCTCT 900  
 QY 901 CCGAGACTGTGAGATCTCTCTCTCTGATCAATAAAAAATGTAAGTTAATTAATGATGAT 960  
 Db 901 CCGAGACTGTGAGATCTCTCTCTCTGATCAATAAAAAATGTAAGTTAATTAATGATGAT 960

QY 961 AAATGATGATGATTAAGTAATTTCCGTTTAAAGCTGTAATCATTTAGTATCATTTG 1020  
 Db 961 AAATGATGATGATTAAGTAATTTCCGTTTAAAGCTGTAATCATTTAGTATCATTTG 1020  
 QY 1021 GAATATTTTAAATTTCTATATTTTGTTCATATAGGTGCTGTAATGCTGTACTTAT 1080  
 Db 1021 GAATATTTTAAATTTCTATATTTTGTTCATATAGGTGCTGTAATGCTGTACTTAT 1080  
 QY 1081 AAATATGAGGAAATGCTTTTATCAAGTAAGTAATTTTAAACAGTGTATAGCTCTTT 1140  
 Db 1081 AAATATGAGGAAATGCTTTTATCAAGTAAGTAATTTTAAACAGTGTATAGCTCTTT 1140  
 QY 1141 GGTGATGTTGTAGTTTCCCTCCCAAGACATGCTGAGATTTCTTCCCAAGAGAT 1200  
 Db 1141 GGTGATGTTGTAGTTTCCCTCCCAAGACATGCTGAGATTTCTTCCCAAGAGAT 1200  
 QY 1201 TCCACACTGAGTGAAGGTGCTGCTACTCTCCGTCAGTTCTGACTTTCTCACTCTA 1260  
 Db 1201 TCCACACTGAGTGAAGGTGCTGCTACTCTCCGTCAGTTCTGACTTTCTCACTCTA 1260  
 QY 1261 ACGTGTCTGAAATATTAAGCACTGCAATTTATTTTAAAGCAATGATGATGATGAC 1320  
 Db 1261 ACGTGTCTGAAATATTAAGCACTGCAATTTATTTTAAAGCAATGATGATGATGAC 1320  
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 Db 1321 ATTAATAATATTAACAAATGCTTATTAATTAATTTGATGATGATGATGATGATGAT 1380  
 QY 1381 ATATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 Db 1381 ATATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 QY 1441 TATATGCTAAATTAAGTAATTTTAAAGCTGAGATGATGATGATGATGATGATGAT 1500  
 Db 1441 TATATGCTAAATTAAGTAATTTTAAAGCTGAGATGATGATGATGATGATGATGAT 1500  
 QY 1501 TAAATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 1560  
 Db 1501 TAAATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 1560  
 QY 1561 CTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 1620  
 Db 1561 CTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 1620  
 QY 1621 AATATGCTGTGTTTGTGCTAGAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1680  
 Db 1621 AATATGCTGTGTTTGTGCTAGAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1680  
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 Db 1681 TGTAAATACCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1740  
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 Db 1801 GTATACATTTGCAAGATGACAAATTTTATTAACCTGTGATTTATTTGAT 1860  
 QY 1861 TTTTAAATTTTCCATTTAGCAACCACTGTGACCTGATTAAGTATTTGAT 1920  
 Db 1861 TTTTAAATTTTCCATTTAGCAACCACTGTGACCTGATTAAGTATTTGAT 1920  
 QY 1921 CACACTGAGAGTCAACCTGTGCAAGGGGTACTGTGGAAGATATTTCAAAACCTGTC 1980  
 Db 1921 CACACTGAGAGTCAACCTGTGCAAGGGGTACTGTGGAAGATATTTCAAAACCTGTC 1980  
 QY 1981 CTTAATTAAGAAATATCATTTGACGGCCAAAGTAAGTTACACATTTCAATGAGGATAT 2040  
 Db 1981 CTTAATTAAGAAATATCATTTGACGGCCAAAGTAAGTTACACATTTCAATGAGGATAT 2040  
 QY 2041 ATTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100

Db	2041	ATTGTGCTCGGCTGTGGCTATTCTTCTATGGAATGTAGACAGTTTCCTGTAAATACCTATTGTGCA	2100
OY	2101	TTTTTCTTTTTTTCACAGAAAAAGTGTGGAGAAAGACGGAGAGTAAACCAATTCTAG	2160
Db	2101	TTTTTCTTTTTTTCACAGAAAAAGCTGTGGAGAAAGACGGAGAGTAAACCAATTCTAG	2160
OY	2161	ACTACGTGCAGAGAGTTTCTTGGGTAAATGAAACCCGAGTGGATTAATAGAAAGTTGAGACT	2220
Db	2161	ACTACGTGCAGAGAGTTTCTTGGGTAAATGAAACCCGAGTGGATTAATAGAAAGTTGAGACT	2220
OY	2221	AAACTGGTTTTGTTCACAGCCCAAGATTTTTGGAGAGAGACATTTTACTGCAGTGCAGAT	2280
Db	2221	AAACTGGTTTTGTTCACAGCCCAAGATTTTTGGAGAGAGACATTTTACTGCAGTGCAGAT	2280
OY	2281	GAGGGCCAGAAAGAGTCAAGGCTTAATTTTCAATTAATTTAACTTCAGAGGGAAAGTA	2340
Db	2281	GAGGGCCAGAAAGAGTCAAGGCTTAATTTTCAATTAATTTAACTTCAGAGGGAAAGTA	2340
OY	2341	AAATTTTTCAGGCACTACGACACCTTTCGCAAGAAAGCTAAATTTCTTAAATATATTTCAG	2400
Db	2341	AAATTTTTCAGGCACTACGACACCTTTCGCAAGAAAGCTAAATTTCTTAAATATATTTCAG	2400
OY	2401	ATATCACAATCATTAAGAGTATTTTCCGACAGCAAAATGATATATCTTTTTCCTAAATTTA	2460
Db	2401	ATATCACAATCATTAAGAGTATTTTCCGACAGCAAAATGATATATCTTTTTCCTAAATTTA	2460
OY	2461	ACTTAACATTCCTGTAAAAATGCTGTTAACCTAATAGTATTTATGAAATGGTTAAGCAATTT	2520
Db	2461	ACTTAACATTCCTGTAAAAATGCTGTTAACCTAATAGTATTTATGAAATGGTTAAGCAATTT	2520
OY	2521	GGTAAATTAAGTATTTATTTAATGTTATGTTGTCTTAATAAACAATAATAGACACTG	2580
Db	2521	GGTAAATTAAGTATTTATTTAATGTTATGTTGTCTTAATAAACAATAATAGACACTG	2580
OY	2581	TTCAATTTGGTGGGCGCTGTGCTGTACAAATTAACCTTGTGCACAGTCCATTTGAGTAC	2640
Db	2581	TTCAATTTGGTGGGCGCTGTGCTGTGTAGCAATTTGAAGTTGTGCACAGTCCATTTGAGTAC	2640
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Db	2641	ATGGCCAGTTTTGAGAGAAAGGCTGTGAGACATGTGCTAGAGATCCCATTTTCTCTGGAG	2700
OY	2701	AAAGTCTCAAGGTTTCAAGGCAACACACAGAGGTGAATCTTACGACAGGACTTAAGTGGGGA	2760
Db	2701	AAAGTCTCAAGGTTTCAAGGCAACACACAGAGGTGAATCTTACGACAGGACTTAAGTGGGGA	2760
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Db	2761	TGTGGGAGACAGGGACACAGGAGAGGTGAACCTGTTTCTCTCTACAGTAAATATTCAG	2820
OY	2821	AAACCTGGGATGTGAGAGGTTAAATGGTGAAGGAATTAATGAATGAATGTCTGTTCCAGA	2880
Db	2821	AAACCTGGGATGTGAGAGGTTAAATGGTGAAGGAATTAATGAATGAATGTCTGTTCCAGA	2880
OY	2881	TGATTTGTAGACCTAAATATGATTTGTTAAAGTCCCTCGAAGAGGATGTGGAACCTGTAA	2940
Db	2881	TGATTTGTAGACCTAAATATGATTTGTTAAAGTCCCTCGAAGAGGATGTGGAACCTGTAA	2940
OY	2941	CTAGTTTTCTGTCCAGGCTGTGAGAAAGATTTGGACAGATCATCTCAATTCACAGTAAAG	3000
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Db	3121	TTCCCGGGGACAGGCAACACAGGCGGACACATCTCATTTGCTGCTTATGGCTATACA	3180

Db	3121	TTCCCGGGGAGGGGACAGCAGCAGGCGCCAGCAACATCATTCCTGCGCTTATGGCATCA	3180
Qy	3181	GTAGCATCAGTAAAGATTTCTTCTGTTCGATGAAAAAATCTCTCAAGAGATCC	3230
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DEFINITION	gene for human B cell differentiation factor.		
ACCESSION	E01640		
VERSION	E01640.1	GI:2169893	
KEYWORDS	JP 1988185387-A/2.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 3230)		
TITLE	Honshiyu, Y., Takatsu, K. and Eba, S.		
JOURNAL	HOMAN B CELL DIFFERENTIATION FACTOR		
COMMENT	Patent: JP 1988185387-A 2 30-JUL-1988; HONSHIYO YU		
OS	Human		
PN	JP 1988185387-A/2		
PD	30-JUL-1988		
PF	21-SEP-1987 JP 1987236842		
PR	20-SEP-1986 JP 86P 223284		
PI	HONSHIYO YU, TAKATSU KIYOSHI, EBA SEBERINSON PC		
C12N15/00, C07K13/00, C12N5/00, C12P21/02, (C12N5/00, C12R1.91);	CC		
Strandedness: Double;			
CC topology: Linear;			
CC hypothetical: No;			
CC anti-sense: No;			
CC *source: tissue type=fetal liver;			
CC *source: clone=pdKCR-hL-5gene;			
CC Feature is identified by similarity;			
CC Key	Location/Qualifiers		
FT	5'UTR 509..552		
FT	exon 509..696		
FT	intron 697..904		
FT	exon 905..937		
FT	intron 938..1882		
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	/db_xref="taxon:9606"		
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ORIGIN			
Query Match	100.0%; Score 3230; DB 6; Length 3230;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 3230;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ATCCTAATCAAGACCCAGTGAACAGAACTGGACCCGCGCAGGCTTGCGCATTTTTCATTTT	60
Db	1	ATCCTAATCAAGACCCAGTGAACAGAACTGGACCCGCGCAGGCTTGCGCATTTTTCATTTT	60
Qy	61	CAATCAGCTGTTCCACGACATATTTTCAATTTCTTTTAAAGACAGATTAAATCTAGCCACA	120
Db	61	CAATCAGCTGTTCCACGACATATTTTCAATTTCTTTTAAAGACAGATTAAATCTAGCCACA	120
Qy	121	GTCATAGTAGAACAATAGCCGATCTTGAAAAAAAACATTTCCCAATATTATTTATTTAGC	180
Db	121	GTCATAGTAGAACAATAGCCGATCTTGAAAAAAAACATTTCCCAATATTATTTATTTAGC	180
Qy	181	ATAAAAATTTCTTTTAGTGTCTACCTTAATCTTTGTTTGCACACATCTTTTAAAGAGAA	240
Db	181	ATAAAAATTTCTTTTAGTGTCTACCTTAATCTTTGTTTGCACACATCTTTTAAAGAGAA	240

Db 181 ATAAATTCCTGTTAGTGGCTACCTTACTGTTGTCACACACTTTTAAGAGAA 240  
QY 241 GTTAATTTTCGATTTTAAGAAATGCAAAATGTGGGCAATGATGTTAAACCAAGAT 300  
Db 241 GTTAATTTTCGATTTTAAGAAATGCAAAATGTGGGCAATGATGTTAAACCAAGAT 300  
QY 301 CCTTCGTAATAGAAAATGTTTTTAAAGGGGGGAAACAGGATTTTTTATTTAAAGAT 360  
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## RESULT 3

HSBCDIFF1

LOCUS

DEFINITION H.sapiens gene for B cell differentiation factor I. 3230 bp DNA linear PRI 30-MAR-1992

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

Homo sapiens.  
 Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 3230)  
 Honjo, T., Takatu, K. and Severinson, E.  
 Unpublished  
 see X12705 for ph.IL-5-30 cDNA sequence;  
 extent of mRNA is given according ph.IL-5-30 cDNA; Data kindly

## FEATURES

supplied by Devent Biotechnology Abstracts: Patent (EP\_0\_261\_625,  
 20.09.86, JP\_23284/86), T. Honjo.  
 Location/Qualifiers

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## RESULT 4

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VERSION    J03478.1 GI:166338
KEYWORDS   colony stimulating factor; interleukin 5.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
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            Tanabe, T., Konishi, M., Mizuta, T., Noma, T. and Honjo, T.
            Molecular cloning and structure of the human interleukin-5 gene
            J. Biol. Chem. 262 (34), 16580-16584 (1987)
PUBMED     88059042
MEDLINE    2824500
REFERENCE  2 (bases 1 to 3230)
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FEATURES
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DEFINITION	gDNA encoding beta-cell differentiation factor, BCDF.		
ACCESSION	EI3592		
VERSION	EI3592.1 GI:3252397		
KEYWORDS	JP 1997215496-A/2.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
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JOURNAL	Honshiyu, Y., Takatsu, K. and Eba, S. PRODUCTION OF HUMAN B CELL DIFFERENTIATION FACTOR Patent: JP 1997215496-A 2 19-AUG-1997; HONSHIYO YUU		
COMMENT	OS Homo sapiens (human) PN JP 1997215496-A/2 PD 19-AUG-1997 PR 21-SEP-1987 JP 1996206192 PI 20-SEP-1986 JP 86P 223384 PI HONSHIYO YUU, TAKATSU KIYOSHI, EBA SEBERIMSON PC CI2N5/09,A61K38/00,A61K38/00,A61K38/00,C07H21/04,C07K14/47, PC C12N5/10 PC C12P21/02,(C12P21/02,C12N1:91); CC strandedness: Double; CC topology: Linear; CC hypothetical: No; CC anti-sense: No; FH key Location/Qualifiers FT source 1..3230 /organism='Homo sapiens'		

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JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 57186)		
AUTHORS	Ricke,D.O. and Wagner,R.P.		
TITLE	Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System		
JOURNAL	Unpublished		
AUTHORS	3 (bases 1 to 57186)		
JOURNAL	Connolly,K.S., Gunning,K.M., Davis,C.A., Kadner,K., Subramanian,S., Miguel,T., Lewis,K.D., Fridlyand,J., Alcivar,D., Benke,J.A., Bondoc,M., Bowen,E., Chiang,A., Critz,P., Jaklevic,M.A., Lando,K., Lindquist,K., Miller,C., Patel,S., Piscla,C., Riley,B.E., Rojesti,H., Sarmiento,R., Yu.C., Montenegro,M., Moise,H., Blazer,R., Flanagan,J., Stultz,J.L. and Martin,C.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-JAN-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.		
COMMENT	Sequence submitted by: DOE Joint Genome Institute For further information about this sequence, including its location and relationship to other sequences, please visit the sequence archive Website ( <a href="http://www.hgc.lbl.gov/sequence-archive.html">http://www.hgc.lbl.gov/sequence-archive.html</a> ) or send email to <a href="mailto:human@genome.lbl.gov">human@genome.lbl.gov</a> . location/Qualifiers		
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1794 GAAGTATGTAATATGACAAATGGAACAAATGGAACAAATTTTATATCTGTCTGATTA 1853  
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 Db 39642 GAAGTATGTAATATGACAAATGGAACAAATGGAACAAATTTTATATCTGTCTGATTA 39701

1854 TTTGCAATTTTAAAAATTTTCTCATTTAGCACCACTGTGCACTGAAGAAATCTTGACAG 1913  
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1914 GAATGAGCACCTGAGAGATCAAACTGTGCAGAGGGGTACTGTGAAGAATAATTCAAA 1973  
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 AC079320/c 160042 bp DNA linear PRI 14-JUL-2002  
 LOCUS Homo sapiens chromosome 5, clone RP11-729C24, complete sequence.  
 DEFINITION AC079320  
 ACCESSION AC079320  
 VERSION AC079320.9 GI:21747557  
 KEYWORDS HTG.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE Birren, B., Nussbaum, C., and Lander, E.  
 1 (bases 1 to 160042)  
 Homo sapiens chromosome 5, clone RP11-729C24  
 Unpublished  
 2 (bases 1 to 160042)  
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 Anderson, S., Barna, N., Bastien, V., Bede, F., Boguslavsky, L.,  
 Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,  
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
 Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,  
 Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,  
 Graham, L., Grand-Pierre, N., Hagos, B., Heatford, A., Horton, L.,  
 Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Larocque, K.,  
 Lamazares, R., Landers, T., Lehoczeky, J., Levine, R., Lieu, C., Liu, G.,  
 Macdonald, P., Margulis, N., McCarthy, M., McEwan, P., McKernan, K.,  
 McPheters, R., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,  
 Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,  
 O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K.,  
 Pierre, N., Pisanil, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,  
 Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,  
 Sougnaz, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A.,  
 Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,  
 Zimmer, A., and Zody, M.  
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 Submitted (27-AUG-2000) Whitehead Institute/MIT Center for Genome  
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 3 (bases 1 to 160042)  
 Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,  
 Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,  
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A.,  
 Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,  
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,  
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karatas, A., Kells, C., Labocque, K., Lamazares, R.,  
 Landers, T., Lehoczeky, J., Levine, R., Liu, G., Maclean, C.,  
 Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,  
 McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,  
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 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
 Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,  
 Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,  
 Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S.,  
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 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,  
 Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.  
 Direct Submission  
 Submitted (16-FEB-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 4 (bases 1 to 160042)  
 Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,  
 Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,



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QY	660	GCTTCTCACTCATGACCTCTGCTGATAGCCAAAGAGTAATTTCTTTATGATTCCTAC		719
D	154928	GCTTCTCACTCATGACCTCTGCTGATAGCCAAAGAGTAATTTCTTTATGATTCCTAC		154869
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QY	960	AAAAATGATGCATGATTAAGTAAATTTCCGTGTTTAAAGCTGTAATCATTAAGTTATCAT	1019	
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 Db 1859 TTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1916  
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 LOCUS A21910  
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 ACCESSION A21910  
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 QY 1902 AATCTTCAGGATPAGGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1961  
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Db	300	AGAGTAAMACCAATTCCTAGACTACTCTCCAGAACTTCTTGGTATATGAACCCGAGTGC	359
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Db	360	ATAATAGAAAGCTTGAAGCTAAACCTGCTTGTGTCACGCCAAAGATTTTGAAGGAGAAAGC	419
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LOCUS	HUM21DC93Z	3710 bp	DNA
DEFINITION	Homo sapiens (subclone 6_b10 from p1 H21) DNA sequence.		
ACCESSION	L48477		
VERSION	L48477.1	GI:1032380	
KEYWORDS	interleukin gene cluster.		
SOURCE	Homo sapiens (tissue library: Subclones in pOT2 from p1 clone H21)		
ORGANISM	DNA.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
	1 (bases 1 to 3710)		
	Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A., Ericsson,C.L., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M., Mayeda,C.A., Steiert-El Kheir,A. and Palazzolo,M.J.		
TITLE	Sequencing of the Interleukin gene cluster of homo sapiens		
JOURNAL	Unpublished (1995)		
COMMENT	This subclone overlaps H21 3_e10 and H21 6_e5.		
	Sequence submitted by:		
	Human Genome Center		
	Lawrence Berkeley Laboratory		
	Berkeley, CA 94720		
	e-mail: seq@genome.lbl.gov		
	The p1, from which this subclone is derived, is adjacent to p1 (1857).		
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 AUTHORS Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Simionovitch, K.  
 TITLE Ibd-related polymorphisms  
 JOURNAL Patient: WO 0142511-A 606 14-JUN-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Ellipsis  
 Biotherapeutics Corporation (CA)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 AUTHORS Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Simionovitch, K.  
 TITLE Ibd-related polymorphisms  
 JOURNAL Patient: WO 0142511-A 603 14-JUN-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Ellipsis  
 Biotherapeutics Corporation (CA)  
 FEATURES  
 source 1..700  
 location/Qualifiers  
 BASE COUNT 216 a 117 c 133 g 234 t  
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OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 21:16:07 ; Search time 714 Seconds

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Searched: 2185239 segs, 112599159 residues

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Minimum DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	2940	91.0	3241	21	AA120978
6	2940	91.0	3241	21	AA134856
7	2940	91.0	4057	21	AA120980
8	2940	91.0	4057	21	AA134858
9	1171.2	36.3	1395	8	AA171243

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11	686.4	21.3	700	22	AA192591	Human inflammatory
12	640.4	19.8	700	22	AA192593	Human inflammatory
13	627.4	19.4	700	22	AA192592	Human inflammatory
14	626	19.4	5397	22	AB133045	Human immune syste
15	622.4	19.3	700	22	AA192595	Human inflammatory
16	616.4	19.1	5397	24	AB133044	Human immune syste
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19	479.4	14.8	816	21	AA13338	Human low adenosin
20	406.8	12.6	700	22	AA192590	Human adenosine re
21	360	11.1	1328	19	AA160019	Human inflammatory
22	354.4	11.0	700	22	AA192596	Nucleic acid G326c
23	230.4	7.1	838	21	AA144265	Human inflammatory
24	170.4	5.3	385	21	AA143842	Porcine IL-5 DNA.
25	163.6	5.1	444	21	AA168875	Modified human int
26	161.8	5.0	6727	18	AA188014	Modified human int
27	161.8	5.0	6727	18	AA188014	Murine IL-5 cDNA g
28	152.4	4.7	610	21	AA155546	Murine IL-5 nucleo
29	152.4	4.7	610	21	AA155547	Canine interleukin
30	145.8	4.5	402	9	AA181380	Canine interleukin
31	128.6	4.0	381	21	AA168867	Modified human int
32	126.8	3.9	377	19	AA101595	Human interleukin-
33	126.6	3.9	393	21	AA168874	Modified human int
34	125.4	3.9	370	10	AA191647	Synthetic interleu
35	125.4	3.9	375	21	AA168872	Modified human int
36	125.4	3.9	399	21	AA168873	Modified human int
37	124	3.8	520	18	AA150755	Modified human int
38	119.8	3.7	357	21	AA168871	Modified human int
39	118.6	3.7	375	21	AA168868	Modified human int
40	100	3.1	339	17	AA14924	T cell replacing f
41	100	3.1	342	17	AA14923	T cell replacing f
42	100	3.1	348	17	AA14922	T cell replacing f
43	100	3.1	399	19	AA164061	T cell replacing f
44	100	3.1	402	17	AA14921	T cell replacing f
45	100	3.1	481	9	AA180461	Clone 115 contg. D

#### ALIGNMENTS

RESULT 1	ID	AA181381	standard; DNA; 3230 BP.
XX	AA181381;		
AC	04-DEC-1990	(first entry)	
XX			
DE	Entire nucleotide sequence of the human B-cell differentiation factor		
DE	chromosomal gene (3.2kb BamHI fragment).		
XX			
KW	Immunodeficiency disease; cancer therapy; interleukin;		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	exon	553..696	
FT		/*tag= a	
FT		/note="Exon 1"	
FT	exon	905..937	
FT		/*tag= b	
FT		/note="Exon 2"	
FT	exon	1883..2011	
FT		/*tag= c	
FT		/note="Exon 3"	
FT	exon	2118..2216	
FT		/*tag= d	
FT		/note="Exon 4"	
PN	EP261625-A.		

PD 30-MAR-1988.  
 XX 21-SEP-1987; 87EP-0113774.  
 XX 20-SEP-1986; 86JP-0223284.  
 XX (HONJ) HONJO T.  
 PI Honjo T, Takatu K, Severinson E;  
 DR WPI: 1988-085927/13.  
 DR P-PSDB; AAP81056.  
 XX Recombinant human B-cell differentiation factor  
 PT used for diagnosis or treatment of immuno deficiency diseases,  
 PT various infections and cancers  
 XX  
 XX Example; Fig 5(1)-5(4); 35pp; English.  
 XX Nucleotide sequence of the exon portions of the human BCDP chromosomal  
 CC gene completely coincided with the nucleotide sequence of human BCDP  
 CC cDNA (M881380). The BCDP is useful in the diagnosis or treatment of  
 CC e.g. immunodeficiency diseases occurring due to the deficiency of this  
 CC factor in a living body and also in the treatment of various infections  
 CC and cancers.  
 XX  
 XX Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 other;

Query Match 100.0%; Score 3230; DB 9; Length 3230;  
 - Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTAATCAGAGACCCGAGTACAGAGAACTGACCTGACCAAGCTTGACATTCATT 60  
 Db 1 ATCTAATCAGAGACCCGAGTACAGAGAACTGACCTGACCAAGCTTGACATTCATT 60  
 QY 61 CAATCAGTCTCTCCACCACTATTTTCATTTCTTTAAGACAGATTATTCAGCCACA 120  
 Db 61 CAATCAGTCTCTCCACCACTATTTTCATTTCTTTAAGACAGATTATTCAGCCACA 120  
 QY 121 GTCATAGTAGAACAATGCGCATCTTGAAAAAACATTCCTCAATATTATGATTATAGC 180  
 Db 121 GTCATAGTAGAACAATGCGCATCTTGAAAAAACATTCCTCAATATTATGATTATAGC 180  
 QY 181 ATAAATATCTGTTAGTGTCTACCTATATCTTTGTTTGACACATCTTTTAAAGAGAA 240  
 Db 181 ATAAATATCTGTTAGTGTCTACCTATATCTTTGTTTGACACATCTTTTAAAGAGAA 240  
 QY 241 GTTAATTTCTGATTTTAAAGAAATGCAATGCGGCAATGATATTAAACCAAGATT 300  
 Db 241 GTTAATTTCTGATTTTAAAGAAATGCAATGCGGCAATGATATTAAACCAAGATT 300  
 QY 301 CCTCCGTAATAGAAATGTTTTTAAAGGGGGGAAACAGGATTTTATTATTTAAAGAT 360  
 Db 301 CCTCCGTAATAGAAATGTTTTTAAAGGGGGGAAACAGGATTTTATTATTTAAAGAT 360  
 QY 361 AAAAGTAATTTATTTTAAAGATTAAGGCAATGGAACATTTAGTTTCACGATATGCC 420  
 Db 361 AAAAGTAATTTATTTTAAAGATTAAGGCAATGGAACATTTAGTTTCACGATATGCC 420  
 QY 421 ATATTATGCGCATCTCTATCTGATTTAGAAATTAATTCATTTCTTAAGACAGCAAT 480  
 Db 421 ATATTATGCGCATCTCTATCTGATTTAGAAATTAATTCATTTCTTAAGACAGCAAT 480  
 QY 481 AAATGATGAGGAGAGAGCTTGTACTATGACATTTCTTGGCAAGGCAAGAGCAAA 540  
 Db 481 AAATGATGAGGAGAGAGCTTGTACTATGACATTTCTTGGCAAGGCAAGAGCAAA 540  
 QY 541 CGTTTCAGAGCATGAGAGATCTTCTGCAATTTGAGTTGCTAGCTCTTGAGAGCTGCTAC 600  
 Db 541 CGTTTCAGAGCATGAGAGATCTTCTGCAATTTGAGTTGCTAGCTCTTGAGAGCTGCTAC 600  
 QY 601 GTGATGCGCATCCGACAGAAATTCACCAAGTGCATTTGTGAAGAGAGACTTGACACTG 660

Db 601 GTGATGCGCATCCGACAGAAATTCOCACAACTGATTTGTGAAGAGAGCTTGACACTG 660  
 QY 661 CTTTCTACTCATGAACTGCTGATAGCAATGAGGTAATTTCTTTATGATTCCTACA 720  
 Db 661 CTTTCTACTCATGAACTGCTGATAGCAATGAGGTAATTTCTTTATGATTCCTACA 720  
 QY 721 GTCGTAAAGTGCATAGTAATCATTTGTGATGATGCTCTTCTATATATAGATTCGT 780  
 Db 721 GTCGTAAAGTGCATAGTAATCATTTGTGATGATGCTCTTCTATATATAGATTCGT 780  
 QY 781 TATAAATTAATAGATTTGAGACACATTAATGATGATGATGATGATGATGATGATGAT 840  
 Db 781 TATAAATTAATAGATTTGAGACACATTAATGATGATGATGATGATGATGATGATGAT 840  
 QY 841 ATTCTGTTAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 Db 841 ATTCTGTTAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
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 Db 901 CCAGACTGAGAGATTCCTGTTCCGTACATTAATAAGTAAATGATTAATGATGATGAT 960  
 QY 961 AAATGATGAGCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1020  
 Db 961 AAATGATGAGCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1020  
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 Db 1021 GAACATTTAATTTCTATATTTGTTTCTATGATGATGATGATGATGATGATGATGAT 1080  
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 Db 1081 AAATATGAGGAATGATCTTTTATCAAGTGAATGCTTTAAACAGTGTATGAGCTCTTT 1140  
 QY 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGATGCTGACGATTTCTTCCAGAGAT 1200  
 Db 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGATGCTGACGATTTCTTCCAGAGAT 1200  
 QY 1201 TCCACACTGAGAGAGAGTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 Db 1201 TCCACACTGAGAGAGAGTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 QY 1261 ACGTGTCTGAAAAGTATTAGCAACTCAGAAATTAATTTTGAACCAATGATCAGTAGAC 1320  
 Db 1261 ACGTGTCTGAAAAGTATTAGCAACTCAGAAATTAATTTTGAACCAATGATCAGTAGAC 1320  
 QY 1321 ATTAATATATTAACAAATGCGCTATATTAATTAATTTCTGATCTTAAATTAATTA 1380  
 Db 1321 ATTAATATATTAACAAATGCGCTATATTAATTAATTTCTGATCTTAAATTAATTA 1380  
 QY 1381 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 Db 1381 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 QY 1441 TATTAGCTTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1500  
 Db 1441 TATTAGCTTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1500  
 QY 1501 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 Db 1501 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
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 Db 1621 AATATGTTGTTGTTTGTGCTTGAAGAAACAAACAAACAAACAAACAAACAAACAAAC 1680  
 QY 1681 TGTAAATACCAAAACAAAGCTTAATCTTGAGACCAAAATGTTTAATTAATTAATTTT 1740



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Db 1681 TGTAAATACCAAAACAAAGCCTAACTTGTGACCAAAATGTTTATATATTTT 1740
Qy 1741 TTTATATGATGATTTAAAAAGTATATATTTATGTTGTAACAATGATGTTTGAAGTAT 1800
Db 1741 TTTATATGATGATTTAAAAAGTATATATTTATGTTGTAACAATGATGTTTGAAGTAT 1800
Qy 1801 GTATACATTTGCAAGATGACATGACCAATTTTATATCTGCTGATATTTGAT 1860
Db 1801 GTATACATTTGCAAGATGACATGACCAATTTTATATCTGCTGATATTTGAT 1860
Qy 1861 TTTAAAAATTTTCTCATTTTACACCAACTGTGACATGAGAAATCTTTCAAGGAATAG 1920
Db 1861 TTTAAAAATTTTCTCATTTTACACCAACTGTGACATGAGAAATCTTTCAAGGAATAG 1920
Qy 1921 CACACTGGAGATCAAACTGTCAAGGGGGTACTGTGGAAAGACTATTCAAAACCTTGT 1980
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Qy 1981 CTTAAATAAAGAAATCATTTGAGGGCAAAAAGTAACTTACACATCAATGGAAGCTAT 2040
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Db 2041 ATTTGCTGCTGCTGCTGCTATTTCTATGAAATGACAGTTCTGTAATACCTATTTGCA 2100
Qy 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAGAGAGAGTAAACCAATTCCTAG 2160
Db 2101 TTTTCTTTTTCACAGAAAAAGTGTGAGAAAGAGAGAGAGTAAACCAATTCCTAG 2160
Qy 2161 ACTACCTGCAAGATTTCTGCTGTAATGAACACCGAGTGGATATATAAAGTTAGACT 2220
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Db 2221 AAACGTGTTTGTGACGCCAAAGATTTTGGAGAGAGAGACATTTTACTGACGTAGAT 2280
Qy 2281 GAGGGCCAAAGAAAGAGTCAAGGCTTAATTTTCAATATATTTTACTTCAAGGAAAGTA 2340
Db 2281 GAGGGCCAAAGAAAGAGTCAAGGCTTAATTTTCAATATATTTTACTTCAAGGAAAGTA 2340
Qy 2341 AATATTTTCAGCATCTGACATTTTCCAGAAAGCATAAATCTTAAATATATTTAG 2400
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Qy 2401 AATACGAAATCATTAAGATATTTTCTCCAGCAAAATGATATCTTTTCTTATTTA 2460
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Db 2461 ACTTAAACATTTCTGTAATAATGCTGTTAACTTAATAGTATTAAGATGTTT 2520
Qy 2521 GGTAAATTAATTAATTAATGATGTTGCTCTAATAAACAATAAAGAACTG 2580
Db 2521 GGTAAATTAATTAATTAATGATGTTGCTCTAATAAACAATAAAGAACTG 2580
Qy 2581 TTTCAATTTGCTGCTGCTGCTGCTTACATTTTGAAGTTAGCACTGATGATG 2640
Db 2581 TTTCAATTTGCTGCTGCTGCTGCTTACATTTTGAAGTTAGCACTGATGATG 2640
Qy 2641 ATGCCCAATTTTGGAGAAAGGCTGTAGACATGTTGCTGAGCAGTCCCATTTCTGAG 2700
Db 2641 ATGCCCAATTTTGGAGAAAGGCTGTAGACATGTTGCTGAGCAGTCCCATTTCTGAG 2700
Qy 2701 AAGTCTCAAGTTTGAAGGACACAGAGAGTGAAGTGAATGATGAGAGACTTAGGGGA 2760
Db 2701 AAGTCTCAAGTTTGAAGGACACAGAGAGTGAAGTGAATGATGAGAGACTTAGGGGA 2760
Qy 2761 TGTGGGAGACAGGACACAGAGAGTGAAGTGAATGATGAGAGACTTAGGGGA 2820
Db 2761 TGTGGGAGACAGGACACAGAGAGTGAAGTGAATGATGAGAGACTTAGGGGA 2820

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Qy 2821 AACCTGGATGCTCGAAGGTTAAATGTAAGGAAATTAATGATGATGCTTTCCAGA 2880
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Qy 2881 TGATTGTACATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
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Qy 2941 CTAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db 2941 CTAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
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Qy 3061 CATTAACAAAGAGACAGAGATGTAAGGACATGCTGCTGCTGCTGCTGCTGCTGCT 3120
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Qy 3121 TTCCGGGGGAGGCGACAGCAGCGCACAAATCCATTCGCTGCTGCTGCTGCTGCT 3180
Db 3121 TTCCGGGGGAGGCGACAGCAGCGCACAAATCCATTCGCTGCTGCTGCTGCTGCT 3180
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Db 3181 GTAGCATCCTAGAGATTTCTGTTGAGAAACTTCTCTCAAGATCC 3230

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RESULT 2  
AAQ74056  
ID AAQ74056 standard; DNA: 3230 BP.

AAQ74056:

29-JAN-1996 (first entry)

Human Interleukin-5.

Interleukin-5; primer: mRNA; specificity: pharmaceutical; ss.

OS Homo sapiens.

PN JP07123984-A.

PD 16-MAY-1995.

PE 05-NOV-1993; 93JP-0275852.

PR 05-NOV-1993; 93JP-0275852.

PA (HITB) HITACHI CHEM CO LTD.

DR WPI: 1995-211627/28.

PT A primer for the detection and the determ. of a specific messenger

PT RNA - can detect and determine specific mRNA(s) with high

PT reliability

PS Example 22; Page 22-24; 35pp; Japanese.

CC AAQ74056 is the human Interleukin-5 gene. This gene is amplified by  
CC the primers AAQ74031-074032. The primers are used specifically for the  
CC detection and isolation of this sequence. They have the advantage of  
CC high sensitivity and reliability and are useful in the pharmaceutical  
CC industry.

SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 other;

Query Match 100.0%; Score 3230; DB 16; Length 3230;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 3230; Conservative 0; Indels 0; Gaps 0;

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QY 1 ATCCGTAATCAGAGCCCGAGTGAAGAACTGACCCCTGCCAGGCTTGCAATTCATTT 60
Db 1 ATCCGTAATCAGAGCCCGAGTGAAGAACTGACCCCTGCCAGGCTTGCAATTCATTT 60
QY 61 CAATCAGTGTCTCCACACAGTATTTTCAATTTCTTTTAAGACAGATTAACTAGCCACA 120
Db 61 CAATCAGTGTCTCCACACAGTATTTTCAATTTCTTTTAAGACAGATTAACTAGCCACA 120
QY 121 GTCATAGTGAACATAGCCGATCTTGAAGAAAAACATTTCCCAATATTTATGATTTAGC 180
Db 121 GTCATAGTGAACATAGCCGATCTTGAAGAAAAACATTTCCCAATATTTATGATTTAGC 180
QY 181 ATAAATCTGTTAGTGTCTACCTATACCTTTGTTTGACACATCTTTTAAGAGAA 240
Db 181 ATAAATCTGTTAGTGTCTACCTATACCTTTGTTTGACACATCTTTTAAGAGAA 240
QY 241 GTTAATTTTGTGATTTTAAGAAATGCAAAATGTGGGCAATGATTTAAACCCAAAGATT 300
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QY 301 CCTTCCGTAATAGAAAAGTTTAAAGGGGGGAAACAGGATTTTATTTAAAGAT 360
Db 301 CCTTCCGTAATAGAAAAGTTTAAAGGGGGGAAACAGGATTTTATTTAAAGAT 360
QY 361 AAAAGTAATTTATTTTAAAGATATAAGGATTTGAAGAACTTTAGTTTACGATATGCC 420
Db 361 AAAAGTAATTTATTTTAAAGATATAAGGATTTGAAGAACTTTAGTTTACGATATGCC 420
QY 421 ATTATAGGCAATCTCTATCTGATTTGTAGAAATTTATTCATTTCTTCAAGACAGCAAT 480
Db 421 ATTATAGGCAATCTCTATCTGATTTGTAGAAATTTATTCATTTCTTCAAGACAGCAAT 480
QY 481 AAATGACTGGGAGCGAGCTGTGACATGACCTTTCTTGGCAAGGCAAGGCAAGAA 540
Db 481 AAATGACTGGGAGCGAGCTGTGACATGACCTTTCTTGGCAAGGCAAGGCAAGAA 540
QY 541 CGTTTCAGAGCCATGAGAGATCTTCTGCAATTTGAGTTTGTAGCTCTTGGAGCTGCCATC 600
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Db 661 CTCTTACTCATCGAAGCTCTGATAGCCATGAGGATTTTCTTATGATTTCTTACA 720
QY 721 GTCTGTAAGTGCATAGTAACTATTTGTGATGTTCTTACTATATATAGAGATCTGT 780
Db 721 GTCTGTAAGTGCATAGTAACTATTTGTGATGTTCTTACTATATATAGAGATCTGT 780
QY 781 TATAAATTAAGATCTGACACATTAATGATGGGATTAATCAATACCCAGCAAC 840
Db 781 TATAAATTAAGATCTGACACATTAATGATGGGATTAATCAATACCCAGCAAC 840
QY 841 ATTCGTGTAAGTATGATGCTGTGCTGTGTAAGAAATGATTTGATTTCTTCTCT 900
Db 841 ATTCGTGTAAGTATGATGCTGTGCTGTGTAAGAAATGATTTGATTTCTTCTCT 900
QY 901 CCAGACTGTGAGATTTCTGTTCTGTACATTAAGAAATGATTAATTTATGATTTAGTA 960
Db 901 CCAGACTGTGAGATTTCTGTTCTGTACATTAAGAAATGATTAATTTATGATTTAGTA 960
QY 961 AAATGATGCAATGATTAAGTAAATTTCTGTTTAAAGTGAATTCATTTAGTATTCATTTG 1020
Db 961 AAATGATGCAATGATTAAGTAAATTTCTGTTTAAAGTGAATTCATTTAGTATTCATTTG 1020
QY 1021 GAACATTAATTTTCTATATTTTGTTCATATGAGTGTGCTGTGAATGCTGTACTTAT 1080
Db 1021 GAACATTAATTTTCTATATTTTGTTCATATGAGTGTGCTGTGAATGCTGTACTTAT 1080

QY 1081 AAATAGGAATGACTTTTATCAAGTAGAATCCCTTTAAACAGTGTAGGCTCTTT 1140
Db 1081 AAATAGGAATGACTTTTATCAAGTAGAATCCCTTTAAACAGTGTAGGCTCTTT 1140
QY 1141 GGTGATGTTGTAGTTTGGCTTCCCAAGAGCATGCTGTAGAGATTTCTTCCAGAAAGAT 1200
Db 1141 GGTGATGTTGTAGTTTGGCTTCCCAAGAGCATGCTGTAGAGATTTCTTCCAGAAAGAT 1200
QY 1201 TCCACACTGAGTGAAGTGTGCTGTAGTGTCCGCTGACATTTCTGACTCTTCTACTCTA 1260
Db 1201 TCCACACTGAGTGAAGTGTGCTGTAGTGTCCGCTGACATTTCTGACTCTTCTACTCTA 1260
QY 1261 ACSTGTTTCTGAAGATTAAGCACTACAGATTTATTTTGAACCATGATCAGTACAC 1320
Db 1261 ACSTGTTTCTGAAGATTAAGCACTACAGATTTATTTTGAACCATGATCAGTACAC 1320
QY 1321 ATTTAAATATATTAACAATGCTTATTTATTAATTTCTGATTTGATTTAAATATATGACT 1380
Db 1321 ATTTAAATATATTAACAATGCTTATTTATTAATTTCTGATTTGATTTAAATATATGACT 1380
QY 1381 ATATGATGCTGTATGCAATGATTAATGCTGTGCTATTTAAATGTAATATATGACT 1440
Db 1381 ATATGATGCTGTATGCAATGATTAATGCTGTGCTATTTAAATGTAATATATGACT 1440
QY 1441 TATTAGCTTAATTAAGATTAAGCACTACAGTGTAGAACTGATGATGATGAT 1500
Db 1441 TATTAGCTTAATTAAGATTAAGCACTACAGTGTAGAACTGATGATGATGATGAT 1500
QY 1501 TAATGTATATGATTTACATTTCCAAACATTTTTCAGATTTACATTAATTAATGATTAAT 1560
Db 1501 TAATGTATATGATTTACATTTCCAAACATTTTTCAGATTTACATTAATTAATGATTAAT 1560
QY 1561 CTTTATTAAGACCTCAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
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Db 1621 AATATGTGTTGTTGTGCTGTAAGAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1680
QY 1681 TGTAAATACCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1740
Db 1681 TGTAAATACCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1740
QY 1741 TTTAATGATGAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
Db 1741 TTTAATGATGAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
QY 1801 GTATACATTTGACATGACATGACCAATTTTATTAATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 GTATACATTTGACATGACATGACCAATTTTATTAATTAATTAATTAATTAATTAATTAAT 1860
QY 1861 TTTAAATTAATTTCTCATTAGACCACTGTGACATGTAAGAAATCTTCAAGGAATAGG 1920
Db 1861 TTTAAATTAATTTCTCATTAGACCACTGTGACATGTAAGAAATCTTCAAGGAATAGG 1920
QY 1921 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACATTTCAAAACCTGTG 1980
Db 1921 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACATTTCAAAACCTGTG 1980
QY 1981 CTTAATTAAGAAATTAATGATGAGGCGCAAAAGATTAATTAATTAATTAATTAATTAAT 2040
Db 1981 CTTAATTAAGAAATTAATGATGAGGCGCAAAAGATTAATTAATTAATTAATTAATTAAT 2040
QY 2041 ATTTGCTGAGGCTGTGCTATTTCTATGCAATTTGACAGATTTCTGTAATTAATTAATTAAT 2100
Db 2041 ATTTGCTGAGGCTGTGCTATTTCTATGCAATTTGACAGATTTCTGTAATTAATTAATTAAT 2100
QY 2101 TTTTCTTTTTCACAGAAAGATGTGAGAAAGAAAGAGAGAGTAACCAATTTCTAG 2160
Db 2101 TTTTCTTTTTCACAGAAAGATGTGAGAAAGAAAGAGAGAGTAACCAATTTCTAG 2160
QY 2161 ACTACCTGCAAGAGTTCTTGTGTATGATACACGAGTGTATTAAGAAATTTAGACT 2220
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Db 2161 ACTACCTGAGAGGTTCTTGGTATGACACCGAGGAGATTAAGAACTTGAGCT 2220
QY 2221 AAACCTGTTTGTTCAGCCAAAGATTTTGAGAGAGACATTTTACGACGTGAGAT 2280
Db 2221 AAACCTGTTTGTTCAGCCAAAGATTTTGAGAGAGACATTTTACGACGTGAGAT 2280
QY 2281 GAGGGCCAAAGAAAGTCAAGCCCTTAATTTCAATATAATTAATTTTACTCAGGAGAAAGTA 2340
Db 2281 GAGGGCCAAAGAAAGTCAAGCCCTTAATTTCAATATAATTAATTTTACTCAGGAGAAAGTA 2340
QY 2341 AATATTTCAGGCACTGACCTGACCTTGGCCAGAAAGCATTAATTTCTTAATAATTTTTCAG 2400
Db 2341 AATATTTCAGGCACTGACCTGACCTTGGCCAGAAAGCATTAATTTCTTAATAATTTTTCAG 2400
QY 2401 AATATCAGAAATCAATGAGATTTTCTCCAGGCAAAATGATATCTTTTCTTATTTTA 2460
Db 2401 AATATCAGAAATCAATGAGATTTTCTCCAGGCAAAATGATATCTTTTCTTATTTTA 2460
QY 2461 ACTTAACATTTCTGTAATAATGCTGTTACTTAATAGTATTTATGAAGTGAAGATTT 2520
Db 2461 ACTTAACATTTCTGTAATAATGCTGTTACTTAATAGTATTTATGAAGTGAAGATTT 2520
QY 2521 GGTAAATAGTATTTATTTATGTTATGTTGTCTTATTAATAACAAATAGCAACTG 2580
Db 2521 GGTAAATAGTATTTATTTATGTTATGTTGTCTTATTAATAACAAATAGCAACTG 2580
QY 2581 TTCAATTTTCTGCTGACCTCTGCTCCCTTACCAATTTGACAGACAGTCATGAGTAC 2640
Db 2581 TTCAATTTTCTGCTGACCTCTGCTCCCTTACCAATTTGACAGACAGTCATGAGTAC 2640
QY 2641 ATGCCCACTTTGAGAGAGAGGCTGACACATGCTGCTGAGCATCCCATTTCTCTGGAG 2700
Db 2641 ATGCCCACTTTGAGAGAGAGGCTGACACATGCTGCTGAGCATCCCATTTCTCTGGAG 2700
QY 2701 AAGTCTCAAGTGTGCAAGGCAACACAGAGAGTGAAGTGAATGATGAGAGAGCTTAAAGGGGA 2760
Db 2701 AAGTCTCAAGTGTGCAAGGCAACACAGAGAGTGAAGTGAATGATGAGAGAGCTTAAAGGGGA 2760
QY 2761 TGTGGGGAGCAGGAGACACAGGAGAGAGTGAACCTGTTTCTCTCACTATATATCCAG 2820
Db 2761 TGTGGGGAGCAGGAGACACAGGAGAGAGTGAACCTGTTTCTCTCACTATATATCCAG 2820
QY 2821 AACCTGGGATGCTGCAAGGCTAAATGTTGAGGAAATTAATGAATGATGCTTCCCAAGA 2880
Db 2821 AACCTGGGATGCTGCAAGGCTAAATGTTGAGGAAATTAATGAATGATGCTTCCCAAGA 2880
QY 2881 TGATTGTAGAACTAAATAGTGTGAAGTCCCTGGAAGAGAGATGGAAGCTGTAA 2940
Db 2881 TGATTGTAGAACTAAATAGTGTGAAGTCCCTGGAAGAGAGATGGAAGCTGTAA 2940
QY 2941 CTAGGTTCTGCTGACCTGCTGAGAGAAATTTGGCAGATCATCTATGCCAGTATAGAG 3000
Db 2941 CTAGGTTCTGCTGACCTGCTGAGAGAAATTTGGCAGATCATCTATGCCAGTATAGAG 3000
QY 3001 AGGAAGCCAGAAACCTCTCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 3060
Db 3001 AGGAAGCCAGAAACCTCTCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 3060
QY 3061 CATTAACAAAGAGACAGAGACATGTTAGGAGTCCCATTTAGAAAGACTGAGTCCGTA 3120
Db 3061 CATTAACAAAGAGACAGAGACATGTTAGGAGTCCCATTTAGAAAGACTGAGTCCGTA 3120
QY 3121 TTCCCGGGGAGGAGGAGACACAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 3180
Db 3121 TTCCCGGGGAGGAGGAGACACAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAG 3180
QY 3181 GTAGCATCACTAGAGATTTCTTGTGTTGAGAAACTTCTCTCAAGAGATCC 3230
Db 3181 GTAGCATCACTAGAGATTTCTTGTGTTGAGAAACTTCTCTCAAGAGATCC 3230

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RESULT 3

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AAC3725
ID AC3725 standard; DNA; 3230 BP.
AC AC3725;
XX 02-FEB-2001 (first entry)
DT Human IL-5 nucleotide sequence.
DE Human IL-5 nucleotide sequence.
KW Human; interleukin-5; IL-5; signal transduction;
KW antisense oligonucleotide; antileukemic; immunosuppressive; cytostatic;
KW IL-5 receptor; alpha; asthma; eosinophilic syndrome; infection;
KW inflammation; cancer; ds.
XX
OS Homo sapiens.
PN WO200058512-A1.
XX 05-OCT-2000.
PD 17-MAR-2000; 2000WO-US07318.
PF 26-MAR-1999; 99US-0280799.
PR (ISIS-) ISIS PHARM INC.
XX Dean NM, Karras JG, McKay R;
PI WPI: 2000-594648/56.
XX
DR Antisense oligonucleotide compound used to treat asthma and
XX eosinophilic syndrome in humans modulates interleukin-5 signal
XX transduction.
PT
PS Example 22; Page 127-128; 156pp; English.
XX
CC The present sequence was used to design oligonucleotides for antisense
CC modulation of interleukin-5 (IL-5) signal transduction. Oligonucleotides
CC were designed to target nucleic acids encoding IL-5 and IL-5
CC receptor-alpha. The antisense oligonucleotides may be used for the
CC treatment of diseases associated with IL-5 signal transduction, IL-5
CC expression or IL-5 receptor-alpha expression. Such diseases include
CC asthma and eosinophilic syndrome. The oligonucleotides are also useful
CC for research uses and to prevent or delay infection, inflammation or
CC tumour formation.
XX
SO Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 other;
Query Match 100.0%; Score 3230; DB 21; Length 3230;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCCCAATCAAGACCCAGTGAACAGAACTGACCCGCAAGGCTGCAATTTCCATT 60
Db 1 ATCCCAATCAAGACCCAGTGAACAGAACTGACCCGCAAGGCTGCAATTTCCATT 60
QY 61 CAATCACTGCTTCCCAACAGATTTTCAATTTCTTTAAGACAGATTAATAGCCACA 120
Db 61 CAATCACTGCTTCCCAACAGATTTTCAATTTCTTTAAGACAGATTAATAGCCACA 120
QY 121 GTCACTAGTGAACATGACCGGATCTTGAAGAAATTAATCCCATATTTATGATTTAGC 180
Db 121 GTCACTAGTGAACATGACCGGATCTTGAAGAAATTAATCCCATATTTATGATTTAGC 180
QY 181 ATAAATTTCTGTTAGTGTCTTACCTTATACCTTTGTTGACACATCTTTAAGAGAA 240
Db 181 ATAAATTTCTGTTAGTGTCTTACCTTATACCTTTGTTGACACATCTTTAAGAGAA 240
QY 241 GTTAATTTCTGATTTAAGAAATGCAAAATGTGGGCAATGATTAATTAACCAAGATT 300
Db 241 GTTAATTTCTGATTTAAGAAATGCAAAATGTGGGCAATGATTAATTAACCAAGATT 300
QY 301 CTTCCGTAATAGAAATGTTTTTAAGGGGGGAAACAGGATTTTATTTAATAAGAT 360

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Db 301 CCTTCGTAATAGAAATGTTTTAAAGGGGGAACAGGATTTTATATTAATAAGAT 360  
Qy 361 AAAAGTAATTTATTTTATAGATATAGGATTTGAAACATTTAGTTGACATATGCC 420  
Db 361 AAAAGTAATTTATTTTAAAGATATAGGATTTGAAACATTTAGTTGACATATGCC 420  
Qy 421 ATATTTAGGATTCCTATCGATGATGTTAGAAATTTATCTTCCTCAAGAGACAAAT 480  
Db 421 ATATTTAGGATTCCTATCGATGATGTTAGAAATTTATCTTCCTCAAGAGACAAAT 480  
Qy 481 AAATTTGACGAGGACGAGCTCTGTACTATGACATTTCTTTGCCAAAGGACAAAGGAGAA 540  
Db 481 AAATTTGACGAGGACGAGCTCTGTACTATGACATTTCTTTGCCAAAGGACAAAGGAGAA 540  
Qy 541 CGTTTCAGAGCCATGAGAGATGCTTCGATTTGAGTTGCTAGCTCTGAGAGCTGCCATC 600  
Db 541 CGTTTCAGAGCCATGAGAGATGCTTCGATTTGAGTTGCTAGCTCTGAGAGCTGCCATC 600  
Qy 601 GTGTATGACATCCGACAGAAATTTCCCAAGATGATTTGTTGAAGAGACCTTGGCAGCTG 660  
Db 601 GTGTATGACATCCGACAGAAATTTCCCAAGATGATTTGTTGAAGAGACCTTGGCAGCTG 660  
Qy 661 CTTTCTACATGACGACCTGCTGCTGATAGCCAAATGAGGTAATTTCTTTATGATTTCTTACA 720  
Db 661 CTTTCTACATGACGACCTGCTGCTGATAGCCAAATGAGGTAATTTCTTTATGATTTCTTACA 720  
Qy 721 GTCTGTAAAGTCATAGATATCTTTGTATGATGTTCTTACTATATATAGATCTGT 780  
Db 721 GTCTGTAAAGTCATAGATATCTTTGTATGATGTTCTTACTATATATAGATCTGT 780  
Qy 781 TATATAATATATAGATGTCAGACATATAGATGATGATGATGATGATGATGATGATGATGAT 840  
Db 781 TATATAATATATAGATGTCAGACATATAGATGATGATGATGATGATGATGATGATGATGAT 840  
Qy 841 ATTTGTTTAAAGTTATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 ATTTGTTTAAAGTTATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 901 CCAACGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 CCAACGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Qy 961 AAATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
Db 961 AAATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
Qy 1021 GAACATATTTATTTTCTATATTTTGTTCATATGATGATGATGATGATGATGATGATGATGAT 1080  
Db 1021 GAACATATTTATTTTCTATATTTTGTTCATATGATGATGATGATGATGATGATGATGATGAT 1080  
Qy 1081 AAATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
Db 1081 AAATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
Qy 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGATGCTGTCAGAGATTTCTTCCAGAAAGAT 1200  
Db 1141 GGTGATGTTGTTAGTTGCTTCCCAAGAGATGCTGTCAGAGATTTCTTCCAGAAAGAT 1200  
Qy 1201 TCCACACTGAGTGAAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
Db 1201 TCCACACTGAGTGAAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
Qy 1261 ACAGTGTTCGAAAGTATTTAGCACTGAGATTTATTTTGAAGACATGATGATGATGATGATGAT 1320  
Db 1261 ACAGTGTTCGAAAGTATTTAGCACTGAGATTTATTTTGAAGACATGATGATGATGATGATGAT 1320  
Qy 1321 ATTAATAATATATTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
Db 1321 ATTAATAATATATTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
Qy 1381 ATATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
Db 1381 ATATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
|||||  
Db 1381 ATATGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
Qy 1441 TATATGCTAAT 1500  
Db 1441 TATATGCTAAT 1500  
Qy 1501 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
Db 1501 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
Qy 1561 CCTTATTAATACTCCTCAGAT 1620  
Db 1561 CCTTATTAATACTCCTCAGAT 1620  
Qy 1621 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
Db 1621 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
Qy 1681 TGTAAATACCAAAACAAAGGCTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
Db 1681 TGTAAATACCAAAACAAAGGCTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
Qy 1741 TTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
Db 1741 TTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
Qy 1801 GTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
Db 1801 GTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
Qy 1861 TTTTAAATATTTTCTCATATTTTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
Db 1861 TTTTAAATATTTTCTCATATTTTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
Qy 1921 CACACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
Db 1921 CACACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
Qy 1981 CTTAATTAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040  
Db 1981 CTTAATTAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040  
Qy 2041 ATTTGCT 2100  
Db 2041 ATTTGCT 2100  
Qy 2101 TTTTCTTTTTCACAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
Db 2101 TTTTCTTTTTCACAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
Qy 2161 ACTACCTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220  
Db 2161 ACTACCTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220  
Qy 2221 AAATGCTGTTTGTGAGAGCCAAAGATTTTGAAGAGACATTTTACTGACATGATGATGAT 2280  
Db 2221 AAATGCTGTTTGTGAGAGCCAAAGATTTTGAAGAGACATTTTACTGACATGATGATGATGAT 2280  
Qy 2281 GAGGGGCAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
Db 2281 GAGGGGCAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
Qy 2341 AATATTTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
Db 2341 AATATTTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
Qy 2401 ATATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
Db 2401 ATATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
Qy 2461 ACTTAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
Db 2461 ACTTAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520



CC comparing the frequency of the haplotype/pair in a population exhibiting  
CC the trait with that of a reference population. A higher frequency in the  
CC trait population indicates the trait is associated with the haplotype.  
CC The polymorphisms and screened compounds are useful to develop  
CC treatment for diseases associated with IL-5 activity including  
CC inflammatory disorders such as asthma. The present sequence represents  
CC the coding sequence of Interleukin 5 (IL5) as described in the  
CC method of the invention.

XX Sequence 9738 BP; 2808 A; 2015 C; 1982 G; 2933 T; 0 other;

Query Match 91.1%; Score 2941.6; DB 24; Length 9738;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 3192; Conservative 0; Mismatches 19; Indels 29; Gaps 21;

QY 1 ATCCATCAAGACCCAGTACAGACAGTCCGACAGGCTTGGA-TCCTCAT 59  
DB 3532 ATCCATCAAGACCCAGTACAGACAGTCCGACAGGCTTGGA-TCCTCAT 3581  
QY 60 TCAATCACTGCTCCACAGTATTTTCAATTTTAAAGACATTAATCAGCCAC 119  
DB 3582 TCAATCACTGCTCCACAGTATTTTCAATTTTAAAGACATTAATCAGCCAC 3641  
QY 120 AGTATAGTACATAGCCGATCTGAAAAAACAATCCCAATATTATATTAG 179  
DB 3642 AGTATAGTACATAGCCGATCT--GAAAAAACAATCCCAATATTATTTAG 3699  
QY 180 CATTAATTCCTGTTAGTGTCTACCTTATCTTTGTCACACATCTTTAAGAGA 239  
DB 3700 CATTAATTCCTGTTAGTGTCTACCTTATCTTTGTCACACATCTTTAAGAGA 3759  
QY 240 AGTTAATTTCTGATTTTAAAGAAATGTCGAGCAATGATTAACCAAGAT 299  
DB 3760 AGTTAATTTCTGATTTTAAAGAAATGTCGAGCAATGATTAACCAAGAT 3819  
QY 300 TCCTCGTATTAAGAAATGTTTAAAGGGGGAACAGGATTTTATTTAAAGA 359  
DB 3820 TC--TTGTAATTAAGAAATGTTTAAAGGGGGAACAGGATTTTATTTAAAGA 3877  
QY 360 TAAAGTAAATTTTAAAGTATTAAGCAATGGAACATTTAGTTTACAGATATG 419  
DB 3878 TAAAGTAAATTTTAAAGTATTAAGCAATGGAACATTTAGTTTACAGATATG 3937  
QY 420 CATATTAGGATCTCTATCTGATTTGTAAGAAATTTATCTTTCCCAAGACAGCA 479  
DB 3938 CATATTAGGATCTCTATCTGATTTGTAAGAAATTTATCTTTCCCAAGACAGCA 3997  
QY 480 TAAATGAGTGGGAGCAGTCTGTACTATGACCTTTTGGCAAGCAAGCAGAGA 539  
DB 3998 TAAATGAGTGGGAGCAGTCTGTACTATGACCTTTTGGCAAGCAAGCAGAGA 4057  
QY 540 ACGTTTACAGCAGTGAAGATGCTTTCGATTTGATTTGCTAGCTTGGAGCTGCTA 599  
DB 4058 ACGTTTACAGCAGTGAAGATGCTTTCGATTTGATTTGCTAGCTTGGAGCTGCTA 4117  
QY 600 CGGTATGACATCCCAAGAAATTCACCAAGTGAAGTGGTGAAGACCTTGAGCT 659  
DB 4118 CGGTATGACATCCCAAGAAATTCACCAAGTGAAGTGGTGAAGACCTTGAGCT 4177  
QY 660 GCTTCTACTCATGCACTGCTGATAGCCAAAGAGTATTTTCTTATGATCTTAC 719  
DB 4178 GCTTCTACTCATGCACTGCTGATAGCCAAAGAGTATTTTCTTATGATCTTAC 4237  
QY 720 AGCTGTAAGTCAATAGTATCATTTTGTGATGTTCTTTACTATATATAGAGATG 779  
DB 4238 AGCTGTAAGTCAATAGTATCATTTTGTGATGTTCTTTACTATATATAGAGATG 4297  
QY 780 TTATTAATTAATTAATCTGACATTAAGTATTAAGTATTAAGTATTAAGTATTA 839  
DB 4298 TTATTAATTAATTAATCTGACATTAAGTATTAAGTATTAAGTATTAAGTATTA 4357  
QY 840 CATTCGTAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 899  
DB CATTCGTAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG

DB 4358 CATTCGTAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 4417  
QY 900 TCCAGACTGTGAGATTCCTGTTCCGTACATTAAGTATTAAGTATTAAGTATTAAG 959  
DB 4418 TCCAGACTGTGAGATTCCTGTTCCGTACATTAAGTATTAAGTATTAAGTATTAAG 4477  
QY 960 AAAATATGAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1019  
DB 4478 AAAATATGAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 4537  
QY 1020 GGAACATTTATTTTCTATTTTCTGTTTCTATATGAGTGTGATGATGCTGATTA 1079  
DB 4538 GGAACATTTATTTTCTATTTTCTGTTTCTATATGAGTGTGATGATGCTGATTA 4597  
QY 1080 TAAATATGAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1139  
DB 4598 TAAATATGAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 4657  
QY 1140 TGGTATGTTGTTAGTTTCCCTTCCCAAGACATGCTGCA-GGATTCTTCCAGAAAG 1198  
DB 4658 TGGTATGTTGTTAGTTTCCCTTCCCAAGACATGCTGCA-GGATTCTTCCAGAAAG 4716  
QY 1199 ATTCCACATGAGTGAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1258  
DB 4717 ATTCCACATGAGTGAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4776  
QY 1259 TAAAGTGTTCGAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1318  
DB 4777 TAAAGTGTTCGAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 4836  
QY 1319 ACATTAATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1377  
DB 4837 ACATTAATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 4896  
QY 1378 ACTATATGATGTTGTTGTTGCTATTTTAAAGTATTAAGTATTAAGTATTAAGTATTA 1434  
DB 4897 ACTATATGATGTTGTTGTTGCTATTTTAAAGTATTAAGTATTAAGTATTAAGTATTA 4956  
QY 1435 ATAG--TTTATAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1493  
DB 4957 ATAGTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 5016  
QY 1494 ATAGTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1553  
DB 5017 ATAGTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 5076  
QY 1554 GTTATATCTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1613  
DB 5077 GTTATATCTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 5136  
QY 1614 TTATCTTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1673  
DB 5137 TTATCTTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 5196  
QY 1674 GAACATGATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1733  
DB 5197 GAACATGATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 5256  
QY 1734 TTATTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1793  
DB 5257 TTATTTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 5316  
QY 1794 GAAGTATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1853  
DB 5317 GAAGTATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 5376  
QY 1854 TTGATTTTAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1913  
DB 5377 TTGATTTTAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 5436  
QY 1914 GAATAGGACACTGAGAGTCAAACTGTGCAAGGGGATCTGTGGAAGAGTATTAAGTATTAAG 1973  
DB 5437 GAATAGGACACTGAGAGTCAAACTGTGCAAGGGGATCTGTGGAAGAGTATTAAGTATTAAG 5496

QY	1974	ACTGTCCTTATATAAGAAATACATTAGCGCCAAAAGTAAGTTACACACTTCGAATG	2033
Db	5497	ACTGTCTCTATATAAGAAATACATTAGCGCCAAAAGTAAGTTACACACTTCGAATG	5566
QY	2034	AAGCTATATTTGCTCGCTGCTGCTATTTCTATGGAATTGACAGTTTCTCTATTAACCT	20939
Db	5557	AAGCTATATTTGCT - CTGGCGTGTGCTATTTCTATGGAATTGACAGTTTCTCTATTAACCT	5615
QY	2094	ATTGTCATTTTCTTTTTTTTACACAGAAAAAGTGTGGAGAAAAAGACGCGAGCTAAACCA	21533
Db	5616	ATTGTCATTTTCTTTTTTTTACAGAAAAAGTGTGGAGAAAAAGACGCGAGCTAAACCA	56759
QY	2154	TTTCCAGACTACCTGCAGAAAGTTTCTTGTGATATACACCGAGTGGATATACAAAGT	22133
Db	5676	TTTCCAGACTACCTGCAGAAAGTTTCTTGTGATATACACCGAGTGGATATACAAAGT	57355
QY	2214	TGAGACTTAACCTGTTGTGTCAGCCCAAGATTTTGGAGAGAGAGACATTTTACTGAG	22733
Db	5736	TGAGACTTAACCTGTTGTGTCAGCCCAAGATTTTGGAGAGAGAGACATTTTACTGAG	57959
QY	2274	TGAGATATAGGGCCCAAGAAAGACGAGGCCCTTAATTTTCAATATATTTAACTTCAGAG	23333
Db	5796	TGAGATATAGGGCCCAAGAAAGACGAGGCCCTTAATTTTCAATATATTTAACTTCAGAG	58555
QY	2334	GAAAGTAAATATTTTCAGGCACTACTGCACACTTGGCCAGAAAGCATTTAAATTTATAT	23939
Db	5856	GAAAGTAAATATTTTCAGGCACTACTGCACACTTGGCCAGAAAGCATTTAAATTTATAT	59155
QY	2394	ATTTCAGATATACGATCATTTGAAGTATTTTCTCCAGCAAAATTTGATATCTTTTTC	24333
Db	5916	ATTTCAGATATACGATCATTTGAAGTATTTTCTCCAGCAAAATTTGATATCTTTTTC	59759
QY	2454	TTATTTTAACCTTAACATTTCTGTAAATGTCTGTTAACCTATATATATATATGAATGTTA	25133
Db	5976	TTATTTTAACCTTAACATTTCTGTAAATGTCTGTTAACCTATATATATATATGAATGTTA	60355
QY	2514	AGAAATTTGGTAAATTAATATTATTTAATATATGTGTGTCTATAATAACAAAAATAG	25733
Db	6036	AGAAATTTGGTAAATTAATATTATTTAATATATATGTGTGTCTATAATAACAAAAATAG	60955
QY	2574	ACAACCTGTCATATTTGCTGTGCGCTCTGCTTACCATTTTGAAGTTAGCAGACATCAT	26333
Db	6096	ACAACCTGTCATATTTGCTGTGCGCTCTGCTTACCATTTTGAAGTTAGCAGACATCAT	61533
QY	2634	TGAGTACATGCCACGTTTGGAGGAAGGGTCTGACACATGTGGCTGAGACATCCCATTTTC	26933
Db	6154	TGAGTACATGCCACGTTTGGAGGAAGGGTCTGACACATGTGGCTGAGACATCCCATTTTC	62133
QY	2694	TCTGAGAGAAGCTCAAGGTTGCAAGGCAACACAGAGTGGAAATATCTACAGACACTTA	27533
Db	6214	TCTGAGAGAAGCTCAAGGTTGCAAGGCAACACAGAGTGGAAATATCTACAGACACTTA	62733
QY	2754	GTGGGGATGTGGGGAGCAGGAGACACAGGAGAGGTGAACCTGTGTTCTCTACAGTA	28133
Db	6274	GTGGGGATGTGGGGAGCAGGAGACACAGGAGAGGTGAACCTGTGTTCTCTACAGTA	63333
QY	2814	TATCCACAACCTGGGAGTGTGCAAGGCTTAATGTATAGGAAATATGAATGAATGTGCTT	28733
Db	6334	TATCCACAACCTGGGAGTGTGCAAGGCTTAATGTATAGGAAATATGAATGAATGTGCTT	63932
QY	2874	TCCCAAGA - TGAATGTAGAACATAAATAGAGTTTGAAG - -CTCCCTCGAAGAAAGGAGT -	29299
Db	6393	TCCCAAGACTGATTTGTAAGAACTAAATATAGTGTAAAGCGCTCCCTCGAAGAAAGGCACTG	6452
QY	2930	--GGAACCTGTAACTAGGTTCTCTGCCAGCCTGTGAGAAAGATTTGCGAGATC - ATCTCA	2986
Db	6453	TGGGAACCTGTAACTAGGTTCTCTGCCAGCCTGTGAGAAAGATTTGCGAGATCATCTCA	6512
QY	2987	TTTGGCAATATAGAGAGAACCCAGAAACCTCTCTGCCAAGGCTCGCAGGGTTCTTA - -	3044
Db	6513	TTTGGCAATATAGAGAGAACCCAGAAACCTCTCTGCCAAGGCTCGCAGGGTTCTTAAC	6572

QY	3045	CCACCTGACCCGACACCAATTAACAAAGG-ACAGAGACACA-TGGTAGGGCAGTCCCATTA	3102
Db	6573	CCACCTGACCCGACACCAATTAACAAAGGACAGAGACACTGGTAGGGCAGTCCCATTA	6632
QY	3103	GAAGACACTGAGTTCCTCGTATTTCCC-GGGCAGGGCAGCAGCACGGCCGACAACA-TCCATT	3160
Db	6633	GAAGACACTGAGTTCCTCGTATTTCCCGGGGGCAGGGCAGCACGGCCGACAACACTCCATT	6692
QY	3161	CGCGCTGGCTTATGGCTATCAGAGCATCATAGAGATTCCTCGTGGAGAAACTTC	3220
Db	6693	CTGCCTGCTTATGGCTATCAGAGCATCATAGAGATTCCTCGTGGAGAAACTTC	6752
RESULT 5			
AF20978	AAAF20978 standard; DNA; 3241 BP.		
XX	AAAF20978:		
AC	14-MAR-2001	(first entry)	
XX	Human low adenosine antisense oligonucleotide related sequence #2545.		
XX	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;		
KW	human; airway disorder; bronchoconstriction; lung inflammation;		
KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;		
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;		
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;		
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; ROS;		
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis		
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;		
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;		
KW	cancer; ss.		
OS	Homo sapiens.		
XX	MO20062736-A2.		
PD	26-OCT-2000.		
XX	24-MAR-2000; 2000WO-US08020.		
XX	06-APR-1999; 99US-0127958.		
PR	(UYEC-) UNIV EAST CAROLINA.		
XX	(NYCE/) NYCE J W.		
PA	Nyce JW;		
PI	WPI: 2000-679539/66.		
DR	Low adenosine (A) content antisense oligonucleotides which do not		
PT	trigger adenosine receptors during metabolism, useful e.g. for treating		
PT	cancers and respiratory obstructions -		
XX	Disclosure: Page 787-788; 1592pp; English.		
PS	The present invention describes low adenosine (A) content antisense		
CC	oligonucleotides and compositions (I) comprising them. In the antisense		
CC	oligonucleotides the A is replaced by a 'universal' or alternative base.		
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,		
CC	immunosuppressive, antiasthmatic, hypotensive and cyostatic activities		
CC	The antisense oligonucleotides and (I) can be used to down-regulate the		
CC	expression and or activity of target polypeptides associated with		
CC	lung/respiratory disorders and malignancies, such as stimulating and		
CC	activating peptide factors and transmitters, transcription factors,		
CC	immunoglobulins and antibodies, antibody receptors, cytokines and		
CC	chemokines, endogenously produced specific and non-specific enzymes,		
CC	binding proteins, adhesion molecules and their receptors, cytokine and		
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central		
CC	nervous system (CNS) and peripheral nervous and non-nervous system		
CC	receptors, CNS and peripheral nervous and non-nervous system peptide		
CC	transmitters, defensins, growth factors, vasoactive peptides and		



receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 3241 BP; 1026 A; 546 C; 632 G; 1037 T; 0 other:

Query Match 91.0%; Score 2940; DB 21; Length 3241;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 3191; Conservative 0; Mismatches 20; Indels 29; Gaps 21;

1 ATCCCAATCAAGACCCCGATGAGACAACTGACCCGCAAGCTGGCA-TTCCATT 59  
3 ATCCCAATCAAGACCCCGATGAGACAACTGACCCGCAAGCTGGCA-TTCCATT 62  
60 TCAATCAGCTCTCCACAGATATTTTCAATTTCTTTAAGACAGATTAATCAGCAC 119  
63 TCAATCAGCTCTCCACAGATATTTTCAATTTCTTTAAGACAGATTAATCAGCAC 122  
120 AGCTAGTAGACATAGCCGATCTGAAAAAATCCCAATTTATATGATATTTTAA 179  
123 AGCTAGTAGACATAGCCGATCTGAAAAAATCCCAATTTATATGATATTTTAA 180  
180 CATATAATCTGTTAGAGTCTACCTATCTTTGTTTGCACACATCTTTAAGAGA 239  
181 CATATAATCTGTTAGAGTCTACCTATCTTTGTTTGCACACATCTTTAAGAGA 240  
240 AGTTAATTTCTGATTTTAAAGATGCAAAATGTGGGCAATGATGTATTAACCAAGAT 299  
241 AGTTAATTTCTGATTTTAAAGATGCAAAATGTGGGCAATGATGTATTAACCAAGAT 300  
300 TCCTCCGTAATGAAAAATGTTTTAAAGGGGGAACAGGATTTTATATTAAGA 359  
301 TC-TTCGTAATGAAAAATGTTTTAAAGGGGGAACAGGATTTTATTAAGA 358  
360 TAAAGTAAATTTATTTTAAAGATATTAAGCATTGGAACATTAGTTCCAGATATGC 419  
369 TAAAGTAAATTTATTTTAAAGATATTAAGCATTGGAACATTAGTTCCAGATATGC 418  
420 CATATTAAGCATCTCTATCTGATGTTGAATTAATTCATTTCTCAAGACAGACAA 479  
419 CATATTAAGCATCTCTATCTGATGTTGAATTAATTCATTTCTCAAGACAGACAA 478  
480 TAAATGAGTGGGAGCGAGTCTGATGACACTTCTTGGCAAGAGCAAGAGCA 539  
479 TAAATGAGTGGGAGCGAGTCTGATGACACTTCTTGGCAAGAGCAAGAGCA 538  
540 AGCTTTCAGAGCATGAGATGCTCTGATGATGATGATGATGATGATGATGATGAT 599  
539 AGCTTTCAGAGCATGAGATGCTCTGATGATGATGATGATGATGATGATGATGAT 598  
600 CGTGTATGCAATCCCGACAGAAATCCACAGATGATGATGATGATGATGATGATGAT 659  
599 CGTGTATGCAATCCCGACAGAAATCCACAGATGATGATGATGATGATGATGATGAT 658  
660 GCTTCTCTCATGCACTGCTGATGATGCAATGAGATTTTCTTATGATCTCTAC 719  
659 GCTTCTCTCATGCACTGCTGATGATGCAATGAGATTTTCTTATGATCTCTAC 718  
720 AGCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779  
719 AGCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 778  
780 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 839

779 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 838  
840 CATCTGTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 899  
839 CATCTGTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 898  
900 TCCAGACTGAGAGATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 959  
899 TCCAGACTGAGAGATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 958  
960 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019  
959 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1018  
1020 GGAATCTTTAATTTCTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1079  
1019 GGAATCTTTAATTTCTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1078  
1080 TAAATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139  
1079 TAAATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138  
1140 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1198  
1139 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1197  
1199 ATTCCACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1258  
1198 ATTCCACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1257  
1259 TAAAGTGTCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1318  
1258 TAAAGTGTCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1317  
1319 ACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1377  
1318 ACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1376  
1378 ACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1434  
1377 ACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1433  
1435 ATAG-TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1493  
1438 ATAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1492  
1494 ATAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1553  
1498 ATAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1552  
1554 GTTATATCTTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1613  
1553 GTTATATCTTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1612  
1614 TTATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1673  
1618 TTATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1672  
1674 GAATCTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1733  
1678 GAATCTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1732  
1734 TTATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1793  
1733 TTATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1792  
1794 GAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1853  
1798 GAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1852  
1854 TTTCATTTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1913





[illegible][illegible]

QY	1914	GAAATAGGCACTATGAGACATCAAACTGTCAGAGGGGATCTGTGAAAGACTATTCAAA	1973
Dp	1918	GAATAGGACACATGAGAGACAAACGTGCACAGGGGGTACTGTGAAAGACTATTCAAA	1977
QY	1974	ACTGTGCTTAAATATAAATAATACATTGACGGCCAAAATAATAGTTATACACATTCATAG	2033
Dp	1978	ACTGTGCTTAAATATAAATAATACATTGACGGCCAAAATAAGTTATACACATTCATAG	2037
QY	2034	AAGCTATATTTGTCTCGCTGTGCTTATTTCTATGTGAATTTGACAGTTTCTGTATATCT	2093
Dp	2038	AAGCTATATTTGTG - CTGGCTGTGCTTATTTCTATGTGAATTTGACAGTTTCTGTATATCT	2096
QY	2094	ATTGTCAATTTTTCTTTTTTACGAAAAAGTGGAGAAAGAACGGAGATTAACCA	2153
Dp	2097	ATTGTCAATTTTTCTTTTTTACGAAAAAGTGGAGAAAGAACGGAGATTAACCA	2156
QY	2154	TTTCTAGACTACCTGCAGAGATTTCTTGGTGTAATGACACCAGATGATATAGAAAT	2213
Dp	2157	TTTCTAGACTACCTGCAGAGATTTCTTGGTGTAATGACACCAGATGATATAGAAAT	2216
QY	2214	TGAACTAAACTGGTTTGTGTGCGACCCAAAGATTTTGGAGAGACAGACATTTACTGAC	2273
Dp	2217	TGAACTAAACTGGTTTGTGTGCGACCCAAAGATTTTGGAGAGACAGACATTTACTGAC	2276
QY	2274	TGAAATAGAGGGCCAGAAAGAGTCAAGGCTTAATTTCAATATATTAATTACTCAGAG	2333
Dp	2277	TGAAATAGAGGGCCAGAAAGAGTCAAGGCTTAATTTCAATATATTAATTACTCAGAG	2336
QY	2334	GAAAGTAAATATTTTCAGGCACTACTGACACTTTGCCAGAAAGCATAAATTTCTAAATAT	2393
Dp	2337	GAAAGTAAATATTTTCAGGCACTACTGACACTTTGCCAGAAAGCATAAATTTCTAAATAT	2396
QY	2394	ATTTCACATATCAGAAATCATTTGAAGATTTTCTCCAGGCAAAATTTGATATACATTTC	2453
Dp	2397	ATTTCACATATCAGAAATCATTTGAAGATTTTCTCCAGGCAAAATTTGATATACATTTC	2456
QY	2454	TTATTTACTTTAACATTTCTGTAAATGTCTGTAACTTAATAGTATTAATGAATGGTTA	2513
Dp	2457	TTATTTACTTTAACATTTCTGTAAATGTCTGTAACTTAATAGTATTAATGAATGGTTA	2516
QY	2514	AGATTTGGTAATTTAGATTTTAAATGTTATGTGTGTTCTAATTAACAAAAATAG	2573
Dp	2517	AGATTTGGTAATTTAGATTTTAAATGTTATGTGTGTTCTAATTAACAAAAATAG	2576
QY	2574	ACAACCTGTTCAATTTGCTGCTGGCCCTGTGCTTACCAATTTGAAGTTAGCACAGTCCAT	2633
Dp	2577	ACAACCTGTTCAATTTGCTGCTGGCCCTGTGCTTACCAATTTGAAGTTAGCACAGTCCAT	2634
QY	2634	TGATACATCCCAAGTTTGGAGAAAGGTCGTAGCACATGTGGCTAGACATCCCATTTTC	2693
Dp	2635	TGATACATCCCAAGTTTGGAGAAAGGTCGTAGCACATGTGGCTAGACATCCCATTTTC	2694
QY	2694	TCTGGAAGATCTCAAGTTTGCAGAGCACACAGAGAGTGAAGTATCTACAGACTTA	2753
Dp	2695	TCTGGAAGATCTCAAGTTTGCAGAGCACACAGAGAGTGAAGTATCTACAGACTTA	2754
QY	2754	GTTGGGATGTGGGGAGCAGGACACAGGCGAGAGGTGAACCTGTGTTTTCTCTACAGTA	2813
Dp	2755	GTTGGGATGTGGGGAGCAGGACACAGGCGAGAGGTGAACCTGTGTTTTCTCTACAGTA	2814
QY	2814	TATTCACAACTCGAGATGTGTCGAAAGGGTAAATGTATAGGAATTAATGAATGATGTGTT	2873
Dp	2815	TATTCACAACTCGAGATGTG - GAGGGTAAATGTATAGGAATTAATGAATGATGTGTT	2873
QY	2874	TCCAAAG - TGAATGTAGAACTAAATGAAGTTTAG - CTCCCTGGAAGAGGATGT -	2929
Dp	2874	TCCAAAGACTATTTGTGAAGCTAAATGAAGTTTAGAGGCTCCCTGGAAGAGGAGTG	2933
QY	2930	- - GGAACCTGTAACCTAGTTTCCGCGCCACGCTGAGAAATTTGGCAGATC - ATCTCA	2966
Dp	2934	TGGAGACCTGTAACCTAGTTTCCGCGCCACGCTGAGAAATTTGGCAGATCATCTCA	2993

QY	2987	TTGCGATATAGAGAGAGGAGACCCGAAACCCCTCTCTCCAGGCTCGAGGGGTTTAA--	3044
Db	2994	TTGCGATATAGAGAGGAGAACCCGAAACCCCTCTCTCCAGGCTCGAGGGGTTTAAAC	3053
QY	3045	CCACCTGACCCGTGCACCATTAACAAAGG-ACAGAGAGACA-TGGTAGGGCAAGTCCCATTA	3102
Db	3054	CCACCTGACCCGTGCACCATTAACAAAGGAGAGAGACACAGTGTAGGGCAAGTCCCATTA	3113
QY	3103	GAAAGACGAGTTCCGATATTTCC-GGGGGACAGGCGACACAGGCGGCAACACA-TCGATT	3160
Db	3114	GAAAGACTGAGTTCCGATATTTCCGGGGGGACAGGCGACACAGGCGGCAACACACTCCATT	3173
QY	3161	CTGCGCTGCTATGCGCTTCAGTAGCATCACTAGAGATTCTTGTTGAGAAAACCTTTC	3220
Db	3174	CTGCGCTGCTATGCGCTATCGTAGCATCACTAGAGATTCTTGTTGAGAAAACCTTTC	3233

RESULT 7	
AAAF20980	
ID	AAAF20980 standard; DNA; 4057 BP
vv	

DT 14-MAR-2001 (first entry)  
 YY

Human low adenosine antisense oligonucleotide related sequence #2547.

KM Low adenosine arylsulfate oligonucleotide; phosphorothioate; allergy;  
 KM human; airway disorder; bronchoconstriction; lung inflammation;  
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KM respiratory obstruction; pulmonary vasoconstriction; impeded respiration;  
 KM surfactant hypoproduction; pulmonary obstruction; asthma; ROS;  
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis/  
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KM cancer; ss.

OS Homo sapiens.

PN WO2000062736-A2

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

PA (UYEC-) UNIV EAST CAROLINA  
PA (UYCE/) NYCE T EXX  
PT Mrs. T.J.XX  
DD  
KDT: 2000-070520Z

**XX**      **Tour de France**

PT trigger adenosine receptors during metabolism, useful e.g. for treating

XX  
Pictou County, P.E.I. 706-700-1503 ext. 111-1

[illegible]

oligonucleotides and compositions (I) comprising them. In the antisense

(I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antipneumatic, hypotensive and autotatic activities

The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polynucleotides associated with

CC Lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, such as stimulation factors

CC immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific serum

CC binding proteins, adhesion molecules and their receptors, cytokine and

chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergies (allergies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impaired respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 other;

Query Match 91.0%; Score 2940; DB 21; Length 4057;

Best Local Similarity 98.5%; Pred. No. 0; Mismatches 20; Indels 29; Gaps 21;

Matches 3191; Conservative 0; Mismatches 20; Indels 29; Gaps 21;

1 ATCTATCAAGACCCAGTGAACAGAACTGACCCCTGCCAAGGCTTGGA-TTTCATT 59  
 3 ATCTATCAAGACCCAGTGAACAGAACTGACCCCTGCCAAGGCTTGGA-TTTCATT 62  
 60 TCATCACTGCTCTCCACAGATATTTTCAATTTCTTTAAGACAGATTAATCTAGCCAC 119  
 63 TCATCACTGCTCTCCACAGATATTTTCAATTTCTTTAAGACAGATTAATCTAGCCAC 122  
 120 AGCATATGATAGACATAGCCAGTCTGAAAAAACAATCCCATATTTATGATTTAG 179  
 123 AGCATATGATAGACATAGCCAGTCTGAAAAAACAATCCCATATTTATGATTTAG 180  
 180 CATATAATCTGTTAGTGTCTACCTTATACCTTTGTTGACACACATCTTTAAGAGA 239  
 181 CATATAATCTGTTAGTGTCTACCTTATACCTTTGTTGACACACATCTTTAAGAGA 240  
 240 AGTAATATTTCTGATTTTAAAGAAATGAGGAGCATGATTTTAAACCAAGAT 299  
 241 AGTAATATTTCTGATTTTAAAGAAATGAGGAGCATGATTTTAAACCAAGAT 300  
 300 TCCTTCGTAATAGAAATGTTTAAAGGAGGAGAAACAGGATTTTATTTAAAGA 359  
 301 TC-TTCGTAATAGAAATGTTTAAAGGAGGAGAAACAGGATTTTATTTAAAGA 358  
 360 TAAAGTAAATTTATTTTAAAGATATAGGATTTGAAACATTTAGTTACAGATATGC 419  
 359 TAAAGTAAATTTATTTTAAAGATATAGGATTTGAAACATTTAGTTACAGATATGC 418  
 420 CATATTAGGATTTCTATCTGATTTGTAATTTATCTTTCTCAAGACAGACA 479  
 419 CATATTAGGATTTCTATCTGATTTGTAATTTATCTTTCTCAAGACAGACA 478  
 480 TAAATGACTGGGAGCAGCTGTTGATGATGACCTTTCTTTGCAAGGCAAGCAGA 539  
 479 TAAATGACTGGGAGCAGCTGTTGATGATGACCTTTCTTTGCAAGGCAAGCAGA 538  
 540 ACGTTTCAGACCCAGGAGATGCTTTCGATTTGATTTGCTACCTGAGAGTGGCTA 599  
 539 ACGTTTCAGACCCAGGAGATGCTTTCGATTTGATTTGCTACCTGAGAGTGGCTA 598  
 600 CGTGTATGATCCACACAGAAATTTCCACAGATGATTTGTTGAAGAGACCTTGACCT 659  
 599 CGTGTATGATCCACACAGAAATTTCCACAGATGATTTGTTGAAGAGACCTTGACCT 658  
 660 GCTTTTACTGATGAACTGCTGATAGCAATGAGGTAATTTTCTTTATGATCTTAC 719  
 659 GCTTTTACTGATGAACTGCTGATAGCAATGAGGTAATTTTCTTTATGATCTTAC 718  
 720 AGTGTGTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 779

719 AGCTGTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778  
 780 TTTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 839  
 779 TTTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 838  
 840 CATTCGTTAAAAAGTATATATGATGATGATGATGATGATGATGATGATGATGATG 899  
 839 CATTCGTTAAAAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATG 898  
 900 TCCAGACTGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 959  
 899 TCCAGACTGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958  
 960 AAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1019  
 959 AAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1018  
 1020 GGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1079  
 1019 GGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1078  
 1080 TAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1139  
 1079 TAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1138  
 1140 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1198  
 1139 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197  
 1199 ATTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1258  
 1198 ATTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257  
 1259 TAAAGTGTGTTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1318  
 1258 TAAAGTGTGTTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1317  
 1319 ACATTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377  
 1318 ACATTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1376  
 1378 ACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1434  
 1377 ACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1433  
 1435 ATAG-TTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1493  
 1438 ATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1492  
 1494 ATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1553  
 1493 ATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1552  
 1554 GTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1613  
 1553 GTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1612  
 1614 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1673  
 1613 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1672  
 1618 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677  
 1617 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1676  
 1674 GAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1733  
 1673 GAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1732  
 1734 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1793  
 1733 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1792  
 1738 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797  
 1794 GAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1853

Db 1798 GAAGTATGTATACATTGCAGAAATGACAAATGACCAATTTTATACCTTGTCTGATTA 1857  
QY 1854 TTTGCAATTTTAAAAATTTTCTCATTTTACAGCACTGTGCACTGAGAAATCTTTGAG 1913  
Db 1858 TTTGCAATTTTAAAAATTTTCTCATTTTACAGCACTGTGCACTGAGAAATCTTTGAG 1917  
QY 1914 GAATAGGACACAGAGAGCAAGCTGCAAGGGGGTCTGTGGAACATTTTAAAA 1973  
Db 1918 GAATAGGACACAGAGAGCAAGCTGCAAGGGGGTCTGTGGAACATTTTAAAA 1977  
QY 1974 ACTTGTCTTAAATAAGAAATATACATTTAGCGCCAAAAGATTAATGATTAATG 2033  
Db 1978 ACTTGTCTTAAATAAGAAATATACATTTAGCGCCAAAAGATTAATGATTAATG 2037  
QY 2034 AACCTATATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2093  
Db 2038 AACCTATATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2096  
QY 2094 ATTGCAATTTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2153  
Db 2097 ATTGCAATTTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2156  
QY 2154 TTTCTAGACTACCTGCAAGAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2213  
Db 2157 TTTCTAGACTACCTGCAAGAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2216  
QY 2214 TGAGACTAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2273  
Db 2217 TGAGACTAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2276  
QY 2274 TGAGAAATGAGGGCCAGAAAGATGAGGCTTAAATTTTAAATTAATTAATTAATTA 2333  
Db 2277 TGAGAAATGAGGGCCAGAAAGATGAGGCTTAAATTTTAAATTAATTAATTAATTA 2336  
QY 2334 GAAAGTAAATTTTTCAGGCACTGACACTTTCGCCAGAAAGCAATTAATTTTAAAT 2393  
Db 2337 GAAAGTAAATTTTTCAGGCACTGACACTTTCGCCAGAAAGCAATTAATTTTAAAT 2396  
QY 2394 ATTTCAGATATCAGATATCAGATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2453  
Db 2397 ATTTCAGATATCAGATATCAGATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2456  
QY 2454 TTATTTAACTAATCTGTAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2513  
Db 2457 TTATTTAACTAATCTGTAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2516  
QY 2514 AGAATTTGTAATTTAGTATTTTAAATGTAATTTTAAATTTTAAATTTTAAATTT 2573  
Db 2517 AGAATTTGTAATTTAGTATTTTAAATGTAATTTTAAATTTTAAATTTTAAATTT 2576  
QY 2574 ACAACGTTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2633  
Db 2577 ACAACGTTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2634  
QY 2634 TGAGTACATGCGCCAGTTTGAGAGAGGCTGCTGAGCAATGTGGCTGAGATCCCATTC 2693  
Db 2635 TGAGTACATGCGCCAGTTTGAGAGAGGCTGCTGAGCAATGTGGCTGAGATCCCATTC 2694  
QY 2694 TCTGAGAGAGTCTCAAGGTTTCAAGGCAACACAGAGGTGAAGTATTCAGAGACTTA 2753  
Db 2695 TCTGAGAGAGTCTCAAGGTTTCAAGGCAACACAGAGGTGAAGTATTCAGAGACTTA 2754  
QY 2754 GTGGGATGTGGGAGACAGGAGACACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 2813  
Db 2755 GTGGGATGTGGGAGACAGGAGACACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 2814  
QY 2814 TATCCAGAACTGGATGTGCGAAGGGTAAATGTTAGGGAATTAATTAATTAATTAAT 2873  
Db 2815 TATCCAGAACTGGATGTGCGAAGGGTAAATGTTAGGGAATTAATTAATTAATTAAT 2873  
QY 2874 TCCAGAACTGGATGTGCGAAGGGTAAATGTTAGGGAATTAATTAATTAATTAATTA 2929  
Db 2874 TCCAGAACTGGATGTGCGAAGGGTAAATGTTAGGGAATTAATTAATTAATTAATTA 2933

QY 2930 --GAACTGTATAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2986  
Db 2934 TGGGAACCTGTAACTAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2993  
QY 2987 TTTGAGATATAG 3044  
Db 2994 TTTGAGATATAG 3053  
QY 3045 CCACCTGACCCCTGACACCTTAAACAAAGG-ACAGAGAGACA-TGGTAAAGGAGTCCCATTA 3102  
Db 3054 CCACCTGACCCCTGACACCTTAAACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 3113  
QY 3103 GAAAGACTGAGTTCCGTATTTCC-6GGGCAAGGAGACACAGGCGCCACAAACA-TCCATT 3160  
Db 3114 GAAAGACTGAGTTCCGTATTTCC-6GGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 3173  
QY 3161 CTGCTGCTTATAGCTATCAGATATCAGATATCAGATATTTCTGTTTAAAGAACTTCTC 3220  
Db 3174 CTGCTGCTTATAGCTATCAGATATCAGATATTTCTGTTTAAAGAACTTCTC 3233

RESULT 8  
AAA34858  
ID AAA34858 standard; DNA; 4057 BP.  
XX  
AC AAA34858;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2547.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US17712.  
XX  
PR 03-AUG-1998; 98US-0095212.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nlyce JW;  
XX  
DR WPI: 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers -  
XX  
PS Disclosure: Page 717-718; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects affect the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,







Query Match 36.3%; Score 1171.2; DB 8; Length 1395;  
 Best Local Similarity 96.7%; Pred. No. 5.7e-216;  
 Matches 1346; Conservative 0; Mismatches 28; Indels 18; Gaps 14;

QY 1842 TTGCTGATTAATTTGATTTTAAAAATTTTCCATTTTACGACCACTGTCGACGTGAAG 1901  
 DB 1 TTGCTGATTAATTTGATTTTAAAAATTTTCCATTTTACGACCACTGTCGACGTGAAG 60  
 QY 1902 AAATCTTCAGGGAATAGGACACTGAGAGTCAAACCTGCGAAGGGGCTACTGTGGAAA 1961  
 DB 61 AAATCTTCAGGGAATAGGACACTGAGAGTCAAACCTGCGAAGGGGCTACTGTGGAAA 120  
 QY 1962 GACTATTCAAAACTTCTCTTATTAAGAAATACATTTAGCGGCCAAAAAAGTAAGTTACA 2021  
 DB 121 GACTATTCAAAACTTCTCTTATTAAGAAATACATTTAGCGGCCAAAAAAGTAAGTTACA 180  
 QY 2022 CACATTCATAGGAAGCTATATTTGTCGCTGCTGCTGCTATTTCTATGAAATGACAGTTT 2081  
 DB 181 CACATTCATAGGAAGCTATATTTGT-CTGGCTGCTGCTATTTCTATGAAATGACAGTTT 239  
 QY 2082 CCGTATTAACCTATGTCATTTTCTTTTTCACAGAAAAAGTGGAGAGAAAGACGG 2141  
 DB 240 CCGTATTAACCTATGTCATTTTCTTTTTCACAGAAAAAGTGGAGAGAAAGACGG 299  
 QY 2142 AGAGTAACCAATTCCTAGACTACCTGCAAGAGTTCTTGTGTAATGAACACCGAGTGG 2201  
 DB 300 AGAGTAACCAATTCCTAGACTACCTGCAAGAGTTCTTGTGTAATGAACACCGAGTGG 359  
 QY 2202 ATATATGAAAGGTTGACACTAAGCTGTTTGTTCAGCCAAAGATTTTGGAGAGAAAGAC 2261  
 DB 360 ATATATGAAAGGTTGACACTAAGCTGTTTGTTCAGCCAAAGATTTTGGAGAGAAAGAC 419  
 QY 2262 ATTTTACTGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2321  
 DB 420 ATTTTACTGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 479  
 QY 2322 TAACTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2381  
 DB 480 TAACTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 539  
 QY 2382 TTCTTAAATATATTTTCAATATCAGAAATATGAAATATTTTCTTCAGGCAAAATTTGA 2441  
 DB 540 TTCTT-AAAATATATTTTCAATATCAGAAATATGAAATATTTTCTTCAGGCAAAATTTGA 598  
 QY 2442 TATACCTTTTCTTATTTTAACTTAACATTCCTGTAATAATGCTGTTTAACTTAATGATTT 2501  
 DB 599 TATACCTTTTCTTATTTTAACTTAACATTCCTGTAATAATGCTGTTTAACTTAATGATTT 658  
 QY 2502 ATGAATGTTTAAAGATTTGTAATTTAGTATTTTAAATGTTATGTTGTTCTTAATA 2561  
 DB 659 ATGAATGTTTAAAGATTTGTAATTTAGTATTTTAAATGTTATGTTGTTCTTAATA 718  
 QY 2562 AAACAAAAAATAGCAACTGTTCAATTTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2621  
 DB 719 AAACAAAAAATAGCAACTGTTCAATTTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777  
 QY 2622 AGCAGATTCATTTGAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2681  
 DB 778 AGCAGATTCATTTGAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837  
 QY 2682 CATTCCCATTTCTCTGAGAGATCTCAAGGTTCAAGGACACACAGAGTGTGAAGTATC 2741  
 DB 838 CATTCCCATTTCTCTGAGAGATCTCAAGGTTCAAGGACACACAGAGTGTGAAGTATC 896  
 QY 2742 TAGAGAGACTTAGTGGGAGATGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2801  
 DB 897 TAGAGAGACTTAGTGGGAGATGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 956  
 QY 2802 CTCTCTACATTTATATCAGAACTGGGATGTTGGAAGGGTAAATGGAAGGATTAATGTA 2861  
 DB 957 CTCTCTACATTTATATCAGAACTGGGATGTT-GCAGGGTAAATGGAAGGATTAATGTA 1015  
 QY 2862 ATGAATGTCGTTTCAAGA-TGATTTGTAAGTAAATGAGTTGTAAAG-CTCCCTGTGA 2918

DB 1016 ATGATGTCCTTCCAAAGACATGTTGTAAGTAAATGAGATTTGAAGGCTCCCTGGA 1075  
 QY 2919 AGAAGGAGT--GGAACCTGTAACTAGTTCCTGCCAGCTGTGGAAGAAATTTGGC 2975  
 DB 1076 AGAAGGAGTGTGGGAGACCTGTACTAGTTCCTGCCAGCTGTGGAAGAAATTTGGC 1135  
 QY 2976 AGATC-ATCTATGCTGCTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3034  
 DB 1136 AGATCAATCTATGCTGCTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1195  
 QY 3035 GGGGTTCTTA--CCAGCTGACCTGACCATTAACAAAAG-ACAGAGAGCA-TGTAGG 3090  
 DB 1196 GGGGTTCTTAACCCAGCTGACCATTAACAAAAGAGAGAGAGAGAGAGAGAGGAGG 1255  
 QY 3091 CGAGTCCATTTAGAAAGACTGATTCCTATTTCC-GGGGAGAGGAGGAGGAGGAGGAGG 3149  
 DB 1256 CGAGTCCATTTAGAAAGACTGATTCCTATTTCCGGGGGAGGAGGAGGAGGAGGAGG 1315  
 QY 3150 CAACA-TCCATTCGCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATG 3208  
 DB 1316 CAACACTCATTTGCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATG 1375  
 QY 3209 AGAAACTTCTC 3220  
 DB 1376 AGAAACTTCTC 1387  
 RESULT 10  
 AAH92594  
 ID AAH92594 standard; DNA; 700 BP.  
 XX  
 AC AAH92594;  
 XX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human inflammatory bowel disease related gene fragment IGR1294a.  
 XX  
 KW Human: inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200142511-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US33632.  
 XX  
 PR 10-DEC-1999; 99US-0170257.  
 PR 10-APR-2000; 2000US-0196046.  
 XX  
 PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.  
 PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
 XX  
 PI Daily M, Hudson TJ, Lander ES, Rioux J, Siminovitch K,  
 DR WPT. 2001-367874/38.  
 PT Testing for the presence of polymorphisms associated with inflammatory  
 PT bowel disease, using a hybridization assay -  
 XX  
 PS Disclosure: Page 262; 463pp; English.  
 CC The present invention describes a method for detecting the presence of  
 CC polymorphisms associated with inflammatory bowel diseases such as  
 CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
 CC the presence of genetic polymorphisms associated with inflammatory bowel  
 CC disease and correlating their occurrence with disease states. They may be  
 CC used in this way for phenotypic correlations, forensics, paternity  
 CC testing, medicine and genetic analysis. The present sequence is a gene  
 CC containing a polymorphic site described in the exemplification of the



CC Invention.  
XX Sequence 700 BP; 242 A; 101 C; 137 G; 218 T; 2 other;  
SQ

Query Match 21.3%; Score 687; DB 22; Length 700;  
Best Local Similarity 99.6%; Pred. No. 6.6e-123;  
Matches 698; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1741 TTTATGATGATTTAAAGATATATATTTATTTGTCATATATGATGTTTGAAGTAT 1800  
DB 1 TTTATGATGATTTAAAGATATATATTTATTTGTCATATATGATGTTTGAAGTAT 60  
QY 1801 GTATACATTCGACAGATGACCAATGACCAATTTTATACCTGCTGCTGATTTATTCAT 1860  
DB 61 GTATACATTCGACAGATGACCAATGACCAATTTTATACCTGCTGCTGATTTATTCAT 120  
QY 1861 TTTTAAATTTTCCATTTAGCACCACCTGTCACCTGACCAAGATCTTTCAGGGAATAG 1920  
DB 121 TTTTAAATTTTCCATTTAGCACCACCTGTCACCTGACCAAGATCTTTCAGGGAATAG 180  
QY 1921 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATTTCAAAAACCTTGT 1980  
DB 181 CACACTGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAGACTATTTCAAAAACCTTGT 240  
QY 1981 CTTAATAAGAAATATACATTCAGGCGCAAAAGTTACACACATTCATGGAAGCTAT 2040  
DB 241 CTTAATAAGAAATATACATTCAGGCGCAAAAGTTACACACATTCATGGAAGCTAT 300  
QY 2041 ATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100  
DB 301 ATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359  
QY 2101 TTTTCTTTTTCACGAAAAAGTGTGAGAAAGACGAGAGTAAACCAATTCCTAG 2160  
DB 360 TTTTCTTTTTCACGAAAAAGTGTGAGAAAGACGAGAGTAAACCAATTCCTAG 419  
QY 2161 ACTACCTGCAAGAGTCTTGTGCTGATGACACCGAGTGTGATATGAAAGTTGAGCT 2220  
DB 420 ACTACCTGCAAGAGTCTTGTGCTGATGACACCGAGTGTGATATGAAAGTTGAGCT 479  
QY 2221 AAACCTGTTGTTGTCAGCCCAAGATTTTGGAGAGAGACATTTTACTGCAAGTGAAT 2280  
DB 480 AAACCTGTTGTTGTCAGCCCAAGATTTTGGAGAGAGACATTTTACTGCAAGTGAAT 539  
QY 2281 GAGGCGCAAGAAAGAGTCAAGCCTTAATTTTCAATTAATTTTACTGCAAGGGAAGTA 2340  
DB 540 GAGGCGCAAGAAAGAGTCAAGCCTTAATTTTCAATTAATTTTACTGCAAGGGAAGTA 599  
QY 2341 AATATTTGAGGCACTGACGACCTTTCGCCAGAAAGCATAAATTTCTAAATATTTTTCAG 2400  
DB 600 AATATTTGAGGCACTGACGACCTTTCGCCAGAAAGCATAAATTTCTAAATATTTTTCAG 659  
QY 2401 AATATGAAATCATTTGAAGTATTTTCTCCAGGCAAAATTTGA 2441  
DB 660 AATATGAAATCATTTGAAGTATTTTCTCCAGGCAAAATTTGA 700

RESULT 11  
AAH92591  
ID AAH92591 standard; DNA; 700 BP.  
XX

XX AAH92591;

DT 09-OCT-2001 (first entry)

XX Human inflammatory bowel disease related gene fragment IGR1291a.

XX Human inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

XX chromosome 5q31-33; forensic test; gene therapy; ds.

OS Homo sapiens.

XX

PN WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33632.

XX 10-DEC-1999; 99US-0170257.

XX 10-APR-2000; 2000US-0196046.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX (ELI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI: 2001-367874/38.

XX Testing for the presence of polymorphisms associated with inflammatory

XX bowel disease, using a hybridization assay -

XX Disclosure: Page 261; 463pp; English.

XX The present invention describes a method for detecting the presence of

XX polymorphisms associated with inflammatory bowel diseases such as

XX ulcerative colitis and Crohn's disease. The methods can be used to detect

XX the presence of genetic polymorphisms associated with inflammatory bowel

XX disease and correlating their occurrence with disease states. They may be

XX used in this way for phenotypic correlations, forensic analysis, paternity

XX testing, medicine and genetic analysis. The present sequence is a gene

XX containing a polymorphic site described in the exemplification of the

XX invention.

XX

SQ Sequence 700 BP; 216 A; 117 C; 133 G; 234 T; 0 other;

Query Match 21.3%; Score 686.4; DB 22; Length 700;

Best Local Similarity 99.6%; Pred. No. 8.6e-123;

Matches 699; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 247 TTTGATTTTAAAGAAATGCGAAATGTGGGCAATGATATTAACCAATTCCTCC 306

DB 1 TTTGATTTTAAAGAAATGCGAAATGTGGGCAATGATATTAACCAATTCCTCC 58

QY 307 GTAATAGAAATGTTTAAAGGGGGAACAGGATTTTATTTAAAGATTTAAAGT 366

DB 59 GTAATAGAAATGTTTAAAGGGGGAACAGGATTTTATTTAAAGATTTAAAGT 118

QY 367 AAATTTATTTTAAAGATTAAGGATGGAACATTTAGTTGACGATATGCCATTAAT 426

DB 119 AAATTTATTTTAAAGATTAAGGATGGAACATTTAGTTGACGATATGCCATTAAT 178

QY 427 AGGATTTCTATCTGATGTTTGAATTAATTTCTTCTAAAGACAGACATTAATG 486

DB 179 AGGATTTCTATCTGATGTTTGAATTAATTTCTTCTAAAGACAGACATTAATG 238

QY 487 ACTGGGAGCGAGTCTTACTATGCACTTTCTTCCAAAGGCAAGAGCAAGCTTTC 546

DB 239 ACTGGGAGCGAGTCTTACTATGCACTTTCTTCCAAAGGCAAGAGCAAGCTTTC 298

QY 547 AGAGCCATGAGGATCTTCTGCAATTTGATTTGCTAGCTTGGAGCTGCCCTAGCTAT 606

DB 299 AGAGCCATGAGGATCTTCTGCAATTTGATTTGCTAGCTTGGAGCTGCCCTAGCTAT 358

QY 607 GCCATCCCCACAGAAATTTCCACAGAGTGCATTTGGTGAAGAGACTTGGACTGTTCT 666

DB 359 GCCATCCCCACAGAAATTTCCACAGAGTGCATTTGGTGAAGAGACTTGGACTGTTCT 418

QY 667 ACTCATGCACTCTGCTATAGCAATGAGTAAATTTCTTATGATCCACAGCTGT 726

DB 419 ACTCATGCACTCTGCTATAGCAATGAGTAAATTTCTTATGATCCACAGCTGT 478

QY 727 AAAGTCATAGGTAATTTGTGATGCTTCTTACTATATATAGAGATCTGTTATAA 786

DB 479 AAAGTCATAGGTAATTTGTGATGCTTCTTACTATATATAGAGATCTGTTATAA 538

QY 787 TAAATAGATTCGTGAGCAGATAGTACATGGGTATTAACATACACGCAAAACATTCG 846  
DB 539 TAAATAGATTCGTGAGCAGATAGTACATGGGTATTAACATACACGCAAAACATTCG 598  
QY 847 TTAAGATTCGTGAGCAGATAGTACATGGGTATTAACATACACGCAAAACATTCG 906  
DB 599 TTAAGATTCGTGAGCAGATAGTACATGGGTATTAACATACACGCAAAACATTCG 658  
QY 907 TCTGAGATTCGTGAGCAGATAGTACATGGGTATTAACATACACGCAAAACATTCG 948  
DB 659 TCTGAGATTCGTGAGCAGATAGTACATGGGTATTAACATACACGCAAAACATTCG 700

RESULT 12  
AAH92593  
ID AAH92593 standard; DNA; 700 BP.  
XX  
AC AAH92593;  
XX  
DT 09-OCT-2001 (first entry)  
XX  
DE Human inflammatory bowel disease related gene fragment IGR1293a.  
XX  
KW Human: inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
KW chromosome 5q31-33; forensic test; gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200142511-A2.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000WO-US33632.  
XX  
PR 10-DEC-1999; 99US-0170257.  
PR 10-APR-2000; 2000US-0196046.  
XX  
PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.  
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
XX  
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX WPI; 2001-367874/38.  
XX  
XX Testing for the presence of polymorphisms associated with inflammatory  
XX bowel disease, using a hybridization assay -  
PS Disclosure; Page 262; 463pp; English.  
XX  
XX The present invention describes a method for detecting the presence of  
XX polymorphisms associated with inflammatory bowel diseases such as  
XX ulcerative colitis and Crohn's disease. The methods can be used to detect  
XX the presence of genetic polymorphisms associated with inflammatory bowel  
XX disease and correlating their occurrence with disease states. They may be  
XX used in this way for phenotypic correlations, forensics, paternity  
XX testing, medicine and genetic analysis. The present sequence is a gene  
XX containing a polymorphic site described in the exemplification of the  
XX invention.  
XX  
SQ Sequence 700 BP; 253 A; 98 C; 95 G; 254 T; 0 other;

Query Match 19.8%; Score 640.4; DB 22; Length 700;  
Best Local Similarity 98.4%; Pred. No. 6.1e-114;  
Matches 689; Conservative 0; Mismatches 6; Indels 5; Gaps 4;

QY 1247 TCTTTCACCTCAGTCTGTTCTGAAAGTATAGCAACACCAATTTATTTTGAAC 1306  
DB 1 TCTTTCACCTCAGTCTGTTCTGAAAGTATAGCAACACCAATTTATTTTGAAC 60  
QY 1307 CAGTATCAGTATGATTAATATTAACAATGCCCTATATTAATAA-TTCGACATAC 1365  
DB 61 CAGTATCAGTATGATTAATATTAACAATGCCCTATATTAATTTTGCATAC 120

QY 1366 TAAATATATGATATATATGATGTC--TGATGAT--GAATATGCGGTATATTA 1422  
DB 121 TAAATATATGATATATATGATGTC--TGATGAT--GAATATGCGGTATATTA 180  
QY 1423 AATGTAATATATATAG-TTATATAGCTAAATATATTAACATACAGTATG 1481  
DB 181 AATGTAATATATATAGTTTATATAGCTAAATATATTAACATACAGTATG 240  
QY 1482 AATGTAATATATAGTTTATATAGCTAAATATATTAACATACAGTATG 1541  
DB 241 AATGTAATATATAGTTTATATAGCTAAATATATTAACATACAGTATG 300  
QY 1542 TTAAT 1601  
DB 301 TTAAT 360  
QY 1602 TTTTGAAT 1661  
DB 361 TTTTGAAT 420  
QY 1662 CTTTGAAGAGGAGTATATATATATATATATATATATATATATATATATAT 1721  
DB 421 CTTTGAAGAGGAGTATATATATATATATATATATATATATATATATATAT 480  
QY 1722 TTTTGAAT 1781  
DB 481 TTTTGAAT 540  
QY 1782 ATATGATGTTTGAAGTATATATATATATATATATATATATATATATATAT 1841  
DB 541 ATATGATGTTTGAAGTATATATATATATATATATATATATATATATATATAT 600  
QY 1842 TTTTGAAT 1901  
DB 601 TTTTGAAT 660  
QY 1902 AATCTTTTCAGGAGTATATATATATATATATATATATATATATATATATAT 1941  
DB 661 AATCTTTTCAGGAGTATATATATATATATATATATATATATATATATATAT 700

RESULT 13  
AAH92592  
ID AAH92592 standard; DNA; 700 BP.  
XX  
AC AAH92592;  
XX  
DT 09-OCT-2001 (first entry)  
XX  
DE Human inflammatory bowel disease related gene fragment IGR1292a.  
XX  
KW Human: inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
KW chromosome 5q31-33; forensic test; gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200142511-A2.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000WO-US33632.  
XX  
PR 10-DEC-1999; 99US-0170257.  
PR 10-APR-2000; 2000US-0196046.  
XX  
PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.  
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
XX  
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX WPI; 2001-367874/38.  
XX

XX Testing for the presence of polymorphisms associated with inflammatory  
PT bowel disease, using a hybridization assay -  
XX  
XX  
PS Disclosure; Page 261-262; 463pp; English.  
XX

Db 664 AATAATTTCTAATTTTAAATAATACAAATATATAATATAATTAACCAAAAT 605  
 Qy 300 TCCTCCGTATAGAAATGTTTTTAAAGGGGAAACAGGATTTTATATTAAGA 359  
 Db 604 TC--TTGTAATTAATAATATTTTAAATAAAACAAATAATTTTATTAATAAAA 547  
 Qy 360 TAAAGTAAATTTTATTTTATAGATATAGCATTGGAACATTAGTTCAGATATG 419  
 Db 546 TAAATAATTAATTTTATTTTAAATATTAACATTAATAACATTATTTTACAGATATG 487  
 Qy 420 CATTAATAGCATTCTCTATCTGATGTTAGAAATATATCATTTCCCAAGACAGCAA 479  
 Db 486 CATTAATTAATCTCTATCTATTAATTTTAAATTTATTTTATTTTCTCAAAACAAACAA 427  
 Qy 480 TAAATTCAGTGGGAGGAGTCTGTACTATGCACTTTCTTTGGCAAGGCAACGAGA 539  
 Db 426 TAAATTAATTAATAACGCAATCTTATCTATCTTCTTTTACCAAAACAAACGAGA 367  
 Qy 540 ACCTTTAGAGCCATGAGATGCTTCTGCAATTTGAGTTGCTAGCTTGGAGCTGCTA 559  
 Db 366 ACCTTTCAAAACATTAATAATCTCTACATTTAAATTTTACTTAACTTAACTACTA 307  
 Qy 600 CGGTATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTGAAGACCTTGGCAGT 659  
 Db 306 CGTATTAACATCTCCCAACAAATTTCCCAAAATACATTTAATAAAACCTTAACACT 247  
 Qy 660 GCTTCTACATGCACTGCTGATGATGCAATGAGTAATTTCTTTATGATCTCTAC 719  
 Db 246 ACTTTTCTACATGCACTGCTGATGATGCAATGAGTAATTTCTTTATGATCTCTAC 187  
 Qy 720 AGCTGTAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 779  
 Db 186 AATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 127  
 Qy 780 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 839  
 Db 126 TTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 67  
 Qy 840 CATTCGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 899  
 Db 66 CATTCGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 7  
 Qy 900 TCCAGA 905  
 Db 6 TCCAAA 1  
 RESULT 15  
 AAH92595  
 ID AAH92595 standard; DNA; 700 BP.  
 XX  
 AC AAH92595;  
 XX  
 DT 09-0CT-2001 (first entry)  
 XX  
 DE Human inflammatory bowel disease related gene fragment IGR1295a.  
 XX  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200142511-A2.  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US33632.  
 XX  
 PR 10-DEC-1999; 99US-0170257.  
 PR 10-APR-2000; 2000US-0196046.  
 XX  
 PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.

PA (ELLI-) ELLIPIS BOTHERAPEUTICS CORP.  
 XX  
 PI Daly M, Hudson JV, Lander ES, Rioux J, Siminovich K;  
 XX  
 DR WPI; 2001-367874/38.  
 XX  
 PT Testing for the presence of polymorphisms associated with inflammatory  
 PS bowel disease, using a hybridization assay -  
 XX  
 PS Disclosure; Page 262-263; 463pp; English.  
 XX  
 CC The present invention describes a method for detecting the presence of  
 CC polymorphisms associated with inflammatory bowel diseases such as  
 CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
 CC the presence of genetic polymorphisms associated with inflammatory bowel  
 CC disease and correlating their occurrence with disease states. They may be  
 CC used in this way for phenotypic correlations, forensics, paternity  
 CC testing, medicine and genetic analysis. The present sequence is a gene  
 CC containing a polymorphic site described in the exemplification of the  
 CC invention.  
 XX  
 SO Sequence 700 BP; 220 A; 104 C; 168 G; 207 T; 1 other:  
 Query Match 19.3%; Score 622.4; DB 22; Length 700;  
 Best Local Similarity .97.4%; Pred. No. 1.8e-110;  
 Matches 675; Conservative 0; Mismatches 12; Indels 6; Gaps 4;  
 Qy 2241 AGATTTTGGAG 2300  
 Db 1 AAGATTTTGGAG 60  
 Qy 2301 GCCTTAATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2360  
 Db 61 GCCTTAATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120  
 Qy 2361 ACTTGGCAGAAAG 2420  
 Db 121 ACTTGGCAGAAAG 180  
 Qy 2421 TTTTCTCCAGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2480  
 Db 181 TTTTCTCCAGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 Qy 2481 TCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2540  
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 Qy 2721 ACACAG 2780  
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 Qy 2781 GCAG 2840  
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Page 23

DB 658 AGTTGTAAGCGCTCCCTGGAGAGAGGGCAGTC 690

Search completed: April 23, 2003, 23:42:34  
Job time : 751 secs

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RESULT 2			
5324640-1			
Patent No. 5324640			
APPLICANT: Honjo, Tasuku; Takatsu, Kiyoshi; Severinson, Eva			
TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND			
PROCESS OF PRODUCING SAID FACTOR			
NUMBER OF SEQUENCES: 2			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/07/99,467			
FILING DATE: 21-SEP-1987			
SEQ ID NO.: 1			
LENGTH: 3230			
5324640-1			
Query Match			
Best Local Similarity 100.0%; Score 3230; DB 6; Length 3230;			
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	181	ATAAAAATTCGTGTTAGTGGCTCACCTTATACCTTTGTTTGCACACATCTTTTAAAGAGAA	240
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Db 3181 AATATTTGAGCATATGACACTTTGCCAGAAAGCATATAATTTCTTAATATATATTTTC 3240

RESULT 3  
US-09-839-2  
; Sequence 2, Application US/09079839  
; Patent No. 6048726  
; GENERAL INFORMATION:  
; APPLICANT: Wellman, Joel K.  
; APPLICANT: Karim, Afab S.  
; TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION  
; FILE REFERENCE: 09998/002001  
; CURRENT APPLICATION NUMBER: US/09/079, 839  
; CURRENT FILING DATE: 1998-05-15



TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P. O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/629,643A  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/629,643  
FILING DATE: 09-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Viksnins, Ann S  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 150.167W01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-359-3260  
TELEFAX: 612-359-3263  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6727 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 650...3771  
OTHER INFORMATION: Join 650..730, 1560..1592,  
OTHER INFORMATION: 3468..3596, 3676..3771  
US-08-629-643A-5

Query Match 5.0%; Score 161.8; DB 3; Length 6727;  
Best Local Similarity 71.5%; Pred. No. 1.2e-28;  
Matches 258; Conservative 0; Mismatches 92; Indels 11; Gaps 3;

QY 343 TTTTATTATTTAAAGATTAAGTAAATTTTAAATATTAAGCATTTGGAACAT 402  
DB 382 TATTAAAGACGCAAAAAAATGATTTTGTGAAAGCCAGGCACTGGAACCC 441  
QY 403 TTAGTTTCAGCATATGCCATTATAGCATCTCTATCTGATTTGTAATTAATTCAT 462  
DB 442 TGAGTTTCAGGACTGCTTATTAAGTGTCTCTATCTGATTTGTAATTAATTCAT 501  
QY 463 TCCTCAAGACAGACAAATAATGATGAGGAGCAGCTGTGACTATGACATTTCTTTG 522  
DB 502 TCCTC--AGAGAGAGATAATTAATGCTTGAGGATTCGCGCTGCTGCTTCCTTTG 559  
QY 523 CCAAGGCAAGGAGAAAGCTTTCAGGCAATG--AGATGCTTCTGCAATTTGAAGTTG 579  
DB 560 CTGAAGGCCAGCGCTGAAGACTTCAGATGATGAGAGATGCTTTCAGCACTTGAAGTT 619  
QY 580 CTAGCTCTGGAGCTGCTACGCTGATGCCATCCCAAGAAATTCACCAAGTGCATTG 639  
DB 620 CTGACTCTGAG-----CTGTGCTGGGCCACAGTGCATGAGATTCACAGACAGT 673  
QY 640 GTGAAGAGACCTTGGCACTGCTTTCTACTCATGCAATCTGCTGATGAGCAATGAGTA 699  
DB 674 GTGAAGAGACCTTGGCACTGCTTTCTACTCATGCAATCTGCTGATGAGCAATGAGTA 733  
QY 700 A 700

DB 734 A 734

RESULT 6  
US-09-280-799-1  
Sequence 1, Application US/09280799  
Patent No. 6136503  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: McKay, James G.  
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
FILE REFERENCE: ISPH-0340  
CURRENT APPLICATION NUMBER: US/09/280,799  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Patentlin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 6727  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-280-799-1

Query Match 5.0%; Score 161.8; DB 3; Length 6727;  
Best Local Similarity 71.5%; Pred. No. 1.2e-28;  
Matches 258; Conservative 0; Mismatches 92; Indels 11; Gaps 3;

QY 343 TTTTATTATTTAAAGATTAAGTAAATTTTAAATATTAAGCATTTGGAACAT 402  
DB 382 TATTAAAGACGCAAAAAAATGATTTTGTGAAAGCCAGGCACTGGAACCC 441  
QY 403 TTAGTTTCAGCATATGCCATTATAGCATCTCTATCTGATTTGTAATTAATTCAT 462  
DB 442 TGAGTTTCAGGACTGCTTATTAAGTGTCTCTATCTGATTTGTAATTAATTCAT 501  
QY 463 TCCTCAAGACAGACAAATAATGATGAGGAGCAGCTGTGACTATGACATTTCTTTG 522  
DB 502 TCCTC--AGAGAGAGATAATTAATGCTTGAGGATTCGCGCTGCTGCTTCCTTTG 559  
QY 523 CCAAGGCAAGGAGAAAGCTTTCAGGCAATG--AGATGCTTCTGCAATTTGAAGTTG 579  
DB 560 CTGAAGGCCAGCGCTGAAGACTTCAGATGATGAGAGATGCTTTCAGCACTTGAAGTT 619  
QY 580 CTAGCTCTGGAGCTGCTACGCTGATGCCATCCCAAGAAATTCACCAAGTGCATTG 639  
DB 620 CTGACTCTGAG-----CTGTGCTGGGCCACAGTGCATGAGATTTCCATGAGCACTG 673  
QY 640 GTGAAGAGACCTTGGCACTGCTTTCTACTCATGCAATCTGCTGATGAGCAATGAGTA 699  
DB 674 GTGAAGAGACCTTGGCACTGCTTTCTACTCATGCAATCTGCTGATGAGCAATGAGTA 733  
QY 700 A 700

DB 734 A 734

RESULT 7  
US-09-155-884-5  
Sequence 5, Application US/09155884  
Patent No. 6215040  
GENERAL INFORMATION:  
APPLICANT: James J. Lee et al.  
TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P. O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,884
FILING DATE: Unknown
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/05932
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vlkshins, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 150.167US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
TELEFAX: 612-359-3061
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 650..3771
OTHER INFORMATION: Join 650..730, 1560..1592,
US-09-155-884-5

Query Match
Best Local Similarity 71.5%; Score 161.8; DB 4; Length 6727;
Matches 258; Conservative 0; Mismatches 92; Indels 11; Gaps 3;

QY 343 TTTTATTTTAAAGATAAAGTAAATTTTATTTTAAAGATAAAGCATTTGAAACAT 402
DB 382 TATTAAAGAGCAAAAAAATTCATTTTGTGAAAGCCAGGACGAGAAACCC 441
QY 403 TTATGTTTCAGATATTCATTTAGCATTCCTATTCATTCATTTAGAAATATTCAT 462
DB 442 TGAGTTTCAGGACTGCTTTATTTAGTGTCTCTATTCATTTAGCAATTTATTCAT 501
QY 463 TCTCAAGAGACAGATTAATTTGACTGGAGAGCAGTCTTGTACTATGCACCTTTCTTG 522
DB 502 TCCTC--AGAGAGAGATAATTTGCTTGGGATTCGCCCTGCTGCGCTCTCTCTTG 559
QY 523 CCAAGGCAAGCGAGACGTTTCAGAGCCATG--AGATGCTTCTGCATTTGAGTTTG 579
DB 560 CTGAAGGCGAGCGCTGAGACTTCAGATCATGAGAAAGATGCTTGCACCTGAGTGT 619
QY 580 CTGAGCTTGGAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 639
DB 620 CTGAGCTTCTGAG-----CTGTGCTGAGGCGACCTGATGAGATTTCCATGAGCAG 673
QY 640 GTGAAGAGAGCTTGGAGCTGCTTTTACTATCATGAACTGCTGCTGATGAGCAATGAG 699
DB 674 GTGAAGAGAGCTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
QY 700 A 700
DB 734 A 734

```

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APPLICANT: Shannon, Frances
APPLICANT: Bastiras, Stan
APPLICANT: Hey, Allan W
TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
FILE REFERENCE: 99722
CURRENT APPLICATION NUMBER: US/09/180,864
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 08/591,438
PRIOR FILING DATE: 1994-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 377
TYPE: DNA
ORGANISM: nucleotide sequence encoding modified IL-5
FEATURE:
NAME/KEY: CDS
LOCATION: (4)..(366)
US-09-180-864-1

Query Match
Best Local Similarity 3.9%; Score 126.8; DB 4; Length 377;
Matches 140; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1849 GATTATTTTCAATTTTAAATTTTCTTCATTTAGCACCACACTGTCAGAAATCTT 1908
DB 108 GACTCTGAGGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 167
QY 1909 TCAGGAGATAGGACACTGAGAGAGTCAAACTGTGCAAGGGGCTACTGTGAAAGATTT 1968
DB 168 TCAGGAGATAGGACACTGAGAGAGTCAAACTGTGCAAGGGGCTACTGTGAAAGATTT 227
QY 1969 CAAAACTGCTCTTAAATTAAGAAATATACATTGACGGCCAAA 2010
DB 228 CAAAACTGCTCTTAAATTAAGAAATATACATTGACGGCCAAA 269

RESULT 9
US-08-629-643A-4
Sequence 4, Application US/08629643A
Patent No. 6025539
GENERAL INFORMATION:
APPLICANT: Lee, J. L.
APPLICANT: Lee, N. A.
TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Schwegman, Lundberg, Moessner & Kluth, P. A.
STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,643A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/629,643
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vlkshins, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 150.167W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
TELEFAX: 612-359-3263
TELEX:

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SIMANDEDNESS: SIM  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 FEATURE:

Db 71688 TTTAAAGATGTATACATCTGGAATGGCTAAAG 7165

RESULT 12  
US-08-998-416-288/c  
; Sequence 288, Application US/08998416  
; Patent No. 6239264

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1 GENERAL INFORMATION:
2 APPLICANT: Philippsen, Peter
3 APPLICANT: Pohlmann, Rainer
4 APPLICANT: Steiner, Sabine
5 APPLICANT: Mohr, Christine
6 APPLICANT: Wendland, Jürgen
7 APPLICANT: Knechtle, Philipp
8 APPLICANT: Reibischung, Corline
9 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYII
10 TITLE OF INVENTION: AND USES THEREOF
11 NUMBER OF SEQUENCES: 1152
12 CORRESPONDENCE ADDRESSES:
13 ADDRESS: No. 6239264artis Corporation
14 STREET: 3054 Cornwallis Road
15 CITY: Research Triangle Park
16 STATE: No. 6239264th Carolina
17 COUNTRY: USA
18 ZIP: 27709
19
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: Patentin Release #1.0, Version #1.30
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/998,416
27 FILING DATE: 24-DEC-1997
28 CLASSIFICATION: 435
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: CH 0016/97
31 FILING DATE: 31-DEC-1996
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Meligs, J. Timothy
34 REGISTRATION NUMBER: 38,241
35 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 919-541-8587
38 TELEFAX: 919-541-8689
39 INFORMATION FOR SEQ ID NO: 288:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 837 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: DNA (genomic)
46 ORIGINAL SOURCE:
47 ORGANISM: PAG1241RP
48 US-08-998-416-288
49
50 Query Match 1.8%; Score 59.2; DB 4; Length 837;
51 Best Local Similarity 47.4%; Pred. No. 7.2e-05;
52 Matches 240; Conservative 0; Mismatches 263; Indels 3; Gaps
53
54 QY 1295 TATTTTGAACCATGATCGTAGACATTAAATATATATACAAATGCCCATATATTATTA 1354
55      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
56 Db 558 TAAATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 499
57      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
58 QY 1355 TTTCGCATCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1414
59      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
60 Db 498 TTAATTAATTAAGAAATTTAAAGTTAAATTTAAATTTAAATTAATTTCTTTATTAACATTTAA 439
61      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
62 QY 1415 CAAATTAATAATGTAATAATATATATGTTATTAATGCTAAATAGAAATTAACCTACAGCTAGA 1474
63      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
64 Db 438 AATAATTAATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 379
65      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 QY 1475 ACCTAGAAACACATTCATGATGAGTTAATGTAATATGATTAATGATTTACACTTCACCAAAACATTTT 1534
67      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 Db 378 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 319
69      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 QY 1535 TTTCAGATCTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1594
71      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
72 Db 318 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 259
73      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
74 QY 1595 CATCTACTTTTGAAAATTTTAACTTAATATATGATGCTGTTGTGCTCAGAAAACAAACA 1654

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Db      258  CTAATAATATTTAATTAATTAAT-TTAAATTTGGAACATGACTAAATGATTCATATT 200
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Db      199  AAAATATTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 142
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QY      1715  ACCAAATTTGTTTAATTAATTAATTTTAAATTTGATGCAATTAAGATATATATTTATT 1774
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Db      141  ATAATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 82
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QY      1775  GTGTACATATGATGTTTGAGTAT 1800
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Db      81  GTTAAATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 56
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RESULT 13
US-07-624-313-3
; Sequence 3, Application US/07624313
; Patent No. 5250411
; GENERAL INFORMATION:
; APPLICANT: Ayyanathan, K.
; APPLICANT: Bhat, P.
; APPLICANT: Datta, S.
; APPLICANT: Francis, V.S.N.K.
; APPLICANT: Padmanaban, G.
; APPLICANT: Srinivasa, H.
; TITLE OF INVENTION: NEW ANALYSIS METHOD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/624.313
; FILING DATE: 19901204
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 8904100-8
; FILING DATE: 05-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33, 771
; REFERENCE/DOCKET NUMBER: 1103326-811
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-354-8515
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vivax
; IMMEDIATE SOURCE:
; CLONE: PARC 1153
US-07-624-313-3
Query Match 1.8%; Score 56.6; DB 1; Length 663;
Best Local Similarity 71.8%; Pred. No. 0.00027;
Matches 74; Conservative 0; Mismatches 29; Indels 0; Gaps 0

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Thu Apr 24 08:08:16 2003

us-09-800-629a-78.rni

Page 11

; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-487-826B-13

Query Match	1.7%;	Score 54.6;	DB 2;	length 19124;
Best Local Similarity	46.1%;	Pred. No. 0.0028;		
Matches 257;	Conservative 0;	Mismatches 294;	Indels 6;	Gaps 2

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QY	1309	TGATCAGTACATTTAAATATATATACCAATGCCCTATATATATCTCGCACTTAA	1368
Db	6049	TAAATTAATTTATTTCTCAATATATGCAATATATATATATATATATATATATATAT	6108
QY	1369	ATAATATGACTATATATATGCTGTATATGATTTGAATATGCTGTCATATTTAAATGTA	1428
Db	6109	ATATATATATATATATATGATATGATTTTATATCTATTTTATACAT - GCATTTTATATATTT	6167
QY	1429	AAATATATAGTTTATAGTCTAAATATGAATATAAACACACAGCTAGACGTATGAAACCA	1488
Db	6168	TAGATATACTTTTAAAGATATTTTATATATTTATATATAGTACATATATGATTTTATTA	6227
QY	1489	TTGATATAGTTTATATGATATATATGATTCACCTCCCAACACATTTTTCAGTACATA	1548
Db	6228	TATCAATATTTTCATTTATATATATATATATATATATGACATGACATTTTATATATCTGTA	6287
QY	1549	ATTATGTTATATCCTTTATATATAAACCTCCGAGTATATCATATTAAGCTTCATCTACTTTGA	1608
Db	6288	TTTAAATATATATATTTTATATATATGATTTTACTTAT - - - - TTTTATATATATACA	6342
QY	1609	AAATTTATCTATATATATGCTGCTTTGTTGCTAGAAAACCAACAAAACCTCTTGA	1668
Db	6343	TAAATTTTGAATATCTATTAATATGCAATATACATATATCAAAAAATCCAAACCAATGA	6402
QY	1669	GAAAGCACTCATGTAATATCCACAACAAACAAAGCCCTAACCTTGTGGACCAAAATGTTTT	1728
Db	6403	TAAATCAATTTTATTTTCTGTATTT	6462
QY	1729	ATATATATATTTTATATATGATGAATTTAAACGATATATATATATTTATTTGTCACATATCAT	1788
Db	6463	ATTATATCATTTTATTTTGGTATGCTATATATATATATATATATATATATATATATATATAC	6522
QY	1789	GTTTGAAGTATGATA	1805
Db	6523	AACAAAATTAATATATA	6539

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Job time : 464 secs
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1

2

3

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 22:59:42 ; Search time 335 Seconds

(without alignments)  
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Title: US-09-800-629A-78

Perfect score: 3230

Sequence: 1 atcctaatacaagaccacccagtl.....aaactctcacaagatcc 3230

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3230	100.0	3230	US-09-800-629A-78	Sequence 78, Appl
2	600.6	18.6	1658	US-09-755-633-18	Sequence 18, Appl
3	589.6	18.3	1658	US-09-755-633-19	Sequence 19, Appl
4	205	6.3	671	US-09-755-633-21	Sequence 21, Appl
5	161.8	5.0	6727	US-09-800-629A-1	Sequence 1, Appl
6	152.4	4.7	610	US-09-755-633-4	Sequence 4, Appl
7	152.4	4.7	610	US-09-755-633-6	Sequence 6, Appl
8	99.4	3.1	402	US-09-755-633-7	Sequence 7, Appl
9	99.4	3.1	402	US-09-755-633-8	Sequence 8, Appl
10	90.2	2.8	345	US-09-755-633-9	Sequence 9, Appl
11	90.2	2.8	345	US-09-755-633-11	Sequence 11, Appl
12	61	1.9	32187	US-10-092-154-1550	Sequence 1550, Ap
13	61	1.9	32187	US-09-764-847-1550	Sequence 1550, Ap
14	61	1.9	32193	US-10-092-154-1549	Sequence 1549, Ap
15	61	1.9	32193	US-09-764-847-1549	Sequence 1549, Ap
16	59.4	1.8	99916	US-09-816-095-3	Sequence 3, Appl
17	57.4	1.8	640681	US-09-790-988-1	Sequence 1, Appl
18	57.4	1.8	640681	US-09-790-988-1	Sequence 1, Appl
19	57	1.8	513509	US-09-754-853A-4	Sequence 4, Appl

C 20	55.4	1.7	5917	9	US-10-087-464-9	Sequence 9, Appl
C 21	55	1.7	302250	10	US-09-962-832-154	Sequence 154, Ap
C 22	54.6	1.7	513509	9	US-09-754-853A-4	Sequence 4, Appl
C 23	54	1.7	397658	10	US-09-813-320-3	Sequence 3, Appl
C 24	53.6	1.7	335913	9	US-09-754-853A-2	Sequence 2, Appl
C 25	53.6	1.7	335913	9	US-09-754-853A-3	Sequence 3, Appl
C 26	52	1.6	143068	10	US-09-967-768A-316	Sequence 316, Ap
C 27	51.4	1.6	2000	9	US-09-938-842A-4305	Sequence 4305, Ap
C 28	50.4	1.6	12637	10	US-09-805-458A-3	Sequence 3, Appl
C 29	50.2	1.6	1367	9	US-09-938-842A-4999	Sequence 4999, Ap
C 30	50.2	1.6	1376	9	US-10-011-445-21	Sequence 21, Appl
C 31	50	1.5	1864	9	US-10-105-481-4	Sequence 4, Appl
C 32	49.8	1.5	1803	10	US-09-822-830A-306	Sequence 306, Ap
C 33	49.8	1.5	197496	9	US-09-877-177-10	Sequence 10, Appl
C 34	49.6	1.5	464	9	US-10-046-935-47	Sequence 47, Appl
C 35	49.6	1.5	464	9	US-09-878-178-47	Sequence 47, Appl
C 36	49.6	1.5	464	9	US-10-146-502-47	Sequence 47, Appl
C 37	49.6	1.5	2000	9	US-09-938-842A-3817	Sequence 3817, Ap
C 38	49.2	1.5	2000	9	US-09-938-842A-3652	Sequence 3652, Ap
C 39	49	1.5	12003	10	US-09-764-877-3976	Sequence 3976, Ap
C 40	48.6	1.5	494	9	US-09-918-995-16092	Sequence 16092, A
C 41	48.6	1.5	147309	10	US-09-742-312-3	Sequence 3, Appl
C 42	48.4	1.5	15577	9	US-10-158-160A-8	Sequence 8, Appl
C 43	48.4	1.5	32367	9	US-10-158-160A-14	Sequence 14, Appl
C 44	48.4	1.5	302250	10	US-09-962-832-154	Sequence 154, Ap
C 45	48.4	1.5	684973	10	US-09-263-959-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1.  
US-09-800-629A-78  
Sequence 78, Application US/09800629A  
Patent No. US20020128216A1  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Karas, James G  
APPLICANT: McKay, Robert  
APPLICANT: Manoharan, Nuthiah  
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
FILE REFERENCE: ISPH-0537  
CURRENT APPLICATION NUMBER: US/09/800,629A  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: PCT/US00/07318  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 09/280,799  
NUMBER OF SEQ ID NOS: 210  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 78  
LENGTH: 3230  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-800-629A-78

Query Match 100.0%; Score 3230; DB 10; Length 3230;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCATATCAAGACCCAGTGAACAGAACTGACCCGCAAGGCTTGCAATTCATT 60  
DB 1 ATCCATATCAAGACCCAGTGAACAGAACTGACCCGCAAGGCTTGCAATTCATT 60  
QY 61 CAATCAGCTGCTCCACCAAGTATTTCAATTTCTTTAAGACAGATTAACTAGCCACA 120  
DB 61 CAATCAGCTGCTCCACCAAGTATTTCAATTTCTTTAAGACAGATTAACTAGCCACA 120  
QY 121 GTCAATAGAGAACTAGCCAGTCTTGAAGAAAAAATTTCCCAATATTTAGTATTAGC 180  
DB 121 GTCAATAGAGAACTAGCCAGTCTTGAAGAAAAAATTTCCCAATATTTAGTATTAGC 180

OY	181	ATATAATTCGTGTAGAGGTCACCTTATACCTTGTGTTGGACACATCTTTAAGAGAA	240
Db	181	ATATAATTCGTGTAGAGGTCACCTTATACCTTGTGTTGGACACATCTTTAAGAGAA	240
OY	241	GTTAATTTTCGATTTTAAACAATGCAAAATGCGGGCAATGATGATTAACCCAAAGATT	300
Db	241	GTTAATTTTCGATTTTAAACAATGCAAAATGCGGGCAATGATGATTAACCCAAAGATT	300
OY	301	CCCTCCGTAATAGAAAATGTTTTTAAAGGGGGGAAAACGGATTTTTATATTAACAT	360
Db	301	CCCTCCGTAATAGAAAATGTTTTTAAAGGGGGGAAAACGGATTTTTATATTAACAT	360
OY	361	AAAAGTAAATTTATTTTTTAAGATATTAAGGCAATGGAAACATTTAGTTCCAGATATGCC	420
Db	361	AAAAGTAAATTTATTTTTTAAGATATTAAGGCAATGGAAACATTTAGTTCCAGATATGCC	420
OY	421	ATTATTTAGGCATTCCTCATCTGATGATGTTGAATTTTCATGTTCCCAAAGCAGACAT	480
Db	421	ATTATTTAGGCATTCCTCATCTGATGATGTTGAATTTTCATGTTCCCAAAGCAGACAT	480
OY	481	AAATTTGACTGGGGACGACGATCTTGACTATGCACCTTTCTTGGCCAAAGGCAACGCAAA	540
Db	481	AAATTTGACTGGGGACGACGATCTTGACTATGCACCTTTCTTGGCCAAAGGCAACGCAAA	540
OY	541	CGTTTCAGAGCCATGAGAGATGCTTCGCAATTTGAGTTTGAGTTCTAGCTTGGAGTCCTAC	600
Db	541	CGTTTCAGAGCCATGAGAGATGCTTCGCAATTTGAGTTTGAGTTCTAGCTTGGAGTCCTAC	600
OY	601	GTTGATGCCATCCCCACACGAAATTTCCCAACAAGTCATTTGGTAAAGACACCTTGGCACTG	660
Db	601	GTTGATGCCATCCCCACACGAAATTTCCCAACAAGTCATTTGGTAAAGACACCTTGGCACTG	660
OY	661	CTTTCTACTCATCGACACTGCTGATAGCCAAATGAGATTAATTTCTTATGATTCCTTACA	720
Db	661	CTTTCTACTCATCGACACTGCTGATAGCCAAATGAGATTAATTTCTTATGATTCCTTACA	720
OY	721	GTCGTGTAAGGCAATAGGTAATCATTTGTGATGTTCCCTTACTATATAGAGATCTGT	780
Db	721	GTCGTGTAAGGCAATAGGTAATCATTTGTGATGTTCCCTTACTATATAGAGATCTGT	780
OY	781	TATTAATTAATTAAGATTTGTGACCAATTAGACATTTGGGCTATTAACATCACACAGCAAC	840
Db	781	TATTAATTAATTAAGATTTGTGACCAATTAGACATTTGGGCTATTAACATCACACAGCAAC	840
OY	841	ATTCGTGTAAGGATTAAGATTCGTGTCGTGTCGTAAATAATGATTTGATTTCCCTTCCTCT	900
Db	841	ATTCGTGTAAGGATTAAGATTCGTGTCGTGTCGTAAATAATGATTTGATTTCCCTTCCTCT	900
OY	901	CCACACTCTGAGGATTCCTGTTCTCTGTACATAAAAAATGATTAATTAATTAATGATTCAGTA	960
Db	901	CCACACTCTGAGGATTCCTGTTCTCTGTACATAAAAAATGATTAATTAATTAATGATTCAGTA	960
OY	961	AAATGATGGCATGAATTAAGTAATAATTTCCGTTTAAAGCTGAATACATTAAGTATACATG	1020
Db	961	AAATGATGGCATGAATTAAGTAATAATTTCCGTTTAAAGCTGAATACATTAAGTATACATG	1020
OY	1021	GAACTATTTAAATTTTCAATTTTGTGTTTCAATATGCGTGCGCTGAATGCTGTACTTAT	1080
Db	1021	GAACTATTTAAATTTTCAATTTTGTGTTTCAATATGCGTGCGCTGAATGCTGTACTTAT	1080
OY	1081	AAATATGAGGAATGACTTTTATCAACATGATATCCTTTAACAAGTGAATTAAGGCTCTTT	1140
Db	1081	AAATATGAGGAATGACTTTTATCAACATGATATCCTTTAACAAGTGAATTAAGGCTCTTT	1140
OY	1141	GGTATGTTGTTAGTTTGGCTTCCCAAAGAGCACTGTGTCAGAGATTTCTTCCAGAAAGAT	1200
Db	1141	GGTATGTTGTTAGTTTGGCTTCCCAAAGAGCACTGTGTCAGAGATTTCTTCCAGAAAGAT	1200
OY	1201	TCCACACTGAGATGAGAGTCCGTGCTAGTCCGCTGTCACATTTGACTCTTTCTCAGCTTA	1260
Db	1201	TCCACACTGAGATGAGAGTCCGTGCTAGTCCGCTGTCACATTTGACTCTTTCTCAGCTTA	1260
OY	1261	ACGTGTTTTCGAAAGTATTAAGCACTCAAAATTAATTTTAAACCAATGATCAGTAGAC	1320

Dd	1261	ACGGTCTTCGAAAGTATTGACACTCGACTGATTAATTTTGTGAACCACTGATCGTAC	1320
Qy	1321	ATTAAATATATATAACAATGCCCTATATTAAATTAATCTGCACTCTAAATTAATATGACT	1380
Dd	1321	ATTAAATATATATAACAATGCCCTATATTAAATTAATCTGCACTCTAAATTAATATGACT	1380
Qy	1381	ATATGATGCTGTGTATGATCAATTGAATTCGCTGTCTATTTAAATATGTAATATATAGTT	1440
Dd	1381	ATATGATGCTGTGTATGATCAATTGAATTCGCTGTCTATTTAAATATGTAATATAGTT	1440
Qy	1441	TATTAGCTTAATATGATTAATACTACAGCTGAACTGTAGAAACAACATGTATATGAGTT	1500
Dd	1441	TATTAGCTTAATATGATTAATACTACAGCTGAACTGTAGAAACAACATGTATATGAGTT	1500
Qy	1501	TAAATGTAATATGCAATTCACACTCCAAACAATTTTTTCCAGTTACATTAATTAAGTTATAT	1560
Dd	1501	TAAATGTAATATGCAATTCACACTCCAAACAATTTTTTCCAGTTACATTAATTAAGTTATAT	1560
Qy	1561	CTTTATTAATAAATCTCTCAGTATATCAATTAAGCTTCATCTACTTTTGGAAAATTTATCTT	1620
Dd	1561	CTTTATTAATAAATCTCTCAGTATATCAATTAAGCTTCATCTACTTTTGGAAAATTTATCTT	1620
Qy	1621	AATATNGTGTGTTGTGTGCTGTAAGAAAACAACAAAACCTTTGGAGAGGAACTCA	1680
Dd	1621	AATATNGTGTGTTGTGTGCTGTAAGAAAACAACAAAACCTTTGGAGAGGAACTCA	1680
Qy	1681	TGTAAATACACAAACAAGCCTTAACCTTTGTGAGCAACAATTTGTTTTAATTAATTTAT	1740
Dd	1681	TGTAAATACACAAACAAGCCTTAACCTTTGTGAGCAACAATTTGTTTTAATTAATTTAT	1740
Qy	1741	TTAATGTATGATTAATAAAGTATATATTAATTATGTGTACAAATATGATGTTTGAAGTAT	1800
Dd	1741	TTAATGTATGATTAATAAAGTATATATTAATTATGTGTACAAATATGATGTTTGAAGTAT	1800
Qy	1801	GTAATACATGTGAGATGGAATGGAATGAGCAAAATTTTATACCTGTGCTGATTAATTTGAT	1860
Dd	1801	GTAATACATGTGAGATGGAATGGAATGAGCAAAATTTTATACCTGTGCTGATTAATTTGAT	1860
Qy	1861	TTTTAAAAATTTTCCATCTTATAGCACAACTGTGACATGCAAGAAATCTTTGAGGAAATAG	1920
Dd	1861	TTTTAAAAATTTTCCATCTTATAGCACAACTGTGACATGCAAGAAATCTTTGAGGAAATAG	1920
Qy	1921	CACACTGAGAGTCAAACTGTGCAGAGGGGTACTGTGAAACACATTCAAAACCTTGTCTC	1980
Dd	1921	CACACTGAGAGTCAAACTGTGCAGAGGGGTACTGTGAAACACATTCAAAACCTTGTCTC	1980
Qy	1981	CTTAATATAAGAAATACATTTGACGGCCAAAAGTAACTTACACACATTCMAATGGAAGCTAT	2040
Dd	1981	CTTAATATAAGAAATACATTTGACGGCCAAAAGTAACTTACACACATTCMAATGGAAGCTAT	2040
Qy	2041	ATTTGTCTGTGCTGTGCTATTTCTATGGAATTTGACAGTTTCTGTAACTACTATTTGCA	2100
Dd	2041	ATTTGTCTGTGCTGTGCTATTTCTATGGAATTTGACAGTTTCTGTAACTACTATTTGCA	2100
Qy	2101	TTTTTCTTTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAAACCAATTTCTAG	2160
Dd	2101	TTTTTCTTTTTTTCACAGAAAAAGTGTGAGAGAAAGACGAGAGTAAACCAATTTCTAG	2160
Qy	2161	ACTACCTTGCAAGAGTTCTTGTGTGTATGAAACCGAGTGTGATATAGAAAAGTTGAGACT	2220
Dd	2161	ACTACCTTGCAAGAGTTCTTGTGTGTATGAAACCGAGTGTGATATAGAAAAGTTGAGACT	2220
Qy	2221	AAACGAGTTGTGTCACACCAAGATTTTGGAGAGAGACATTTTACGCACTGTAGAGAT	2280
Dd	2221	AAACGAGTTGTGTCACACCAAGATTTTGGAGAGAGACATTTTACGCACTGTAGAGAT	2280
Qy	2281	GAGGGCAAGAAAGAGTCAAGGCTTAATTTTCAATTAATTTACTTCAGAGGGGAAAGTA	2340
Dd	2281	GAGGGCAAGAAAGAGTCAAGGCTTAATTTTCAATTAATTTACTTCAGAGGGGAAAGTA	2340
Qy	2341	AAATTTTCAGGCAATCTGACACTTTGCGAGAAAGCATAAATTTCTTAAATATATTTTAC	2400
Dd	2341	AAATTTTCAGGCAATCTGACACTTTGCGAGAAAGCATAAATTTCTTAAATATATTTTAC	2400

Db 2341 AATATTGAGCATACCTGACACTTTGCCAGAAAGATATAATTTCTTAATATATTTCAG 2400  
 Oy 2401 AATATGAAATTCATTAAGTATTTTCCAGCAAAATTTGATATATCTTTTCTTATTTA 2460  
 Db 2401 AATATGAAATTCATTAAGTATTTTCCAGCAAAATTTGATATATCTTTTCTTATTTA 2460  
 Oy 2461 ACTTAACTATCTGTAATATGCTGTTAACTTAATATTTTGAATGTTAACTTAATTT 2520  
 Db 2461 ACTTAACTATCTGTAATATGCTGTTAACTTAATATTTTGAATGTTAACTTAATTT 2520  
 Oy 2521 GGTAAATTTAGTATTTTATTTTATGTTTCTTAAATAAATAAATAGACACCTG 2580  
 Db 2521 GGTAAATTTAGTATTTTATTTTATGTTTCTTAAATAAATAAATAGACACCTG 2580  
 Oy 2581 TTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640  
 Db 2581 TTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640  
 Oy 2641 ATGCCAGTTTGGAGAAAGGCTGACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700  
 Db 2641 ATGCCAGTTTGGAGAAAGGCTGACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700  
 Oy 2701 AAGTCTCAAGTTTGAAGGACACACAGAGGTTGAAGTGAATGATGAGAGACTTATGAG 2760  
 Db 2701 AAGTCTCAAGTTTGAAGGACACACAGAGGTTGAAGTGAATGATGAGAGACTTATGAG 2760  
 Oy 2761 TGTGGGAGACAGGACACAGGAGAGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820  
 Db 2761 TGTGGGAGACAGGACACAGGAGAGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820  
 Oy 2821 AACCTGGATGCTGCAAGGTTAAATGTTAGGATTAATGATGATGCTGCTGCTGCTGCTG 2880  
 Db 2821 AACCTGGATGCTGCAAGGTTAAATGTTAGGATTAATGATGATGCTGCTGCTGCTGCTG 2880  
 Oy 2881 TGATTTAGACATAAATAATGTTAGGATTAATGATGATGCTGCTGCTGCTGCTGCTGCTG 2940  
 Db 2881 TGATTTAGACATAAATAATGTTAGGATTAATGATGATGCTGCTGCTGCTGCTGCTGCTG 2940  
 Oy 2941 CTAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000  
 Db 2941 CTAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000  
 Oy 3001 AGGAAGCCGAAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060  
 Db 3001 AGGAAGCCGAAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060  
 Oy 3061 CATTAACAAAGAGACAGAGATGTTAGGAGTCCCTTAAAGAGACTGATGCTGCTGCTG 3120  
 Db 3061 CATTAACAAAGAGACAGAGATGTTAGGAGTCCCTTAAAGAGACTGATGCTGCTGCTG 3120  
 Oy 3121 TTCCCGGGGAGGAGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180  
 Db 3121 TTCCCGGGGAGGAGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180  
 Oy 3181 GTAGCATCTAGAGATTTCTGTTGAGAAATTTCTCTCAAGAGATCC 3230  
 Db 3181 GTAGCATCTAGAGATTTCTGTTGAGAAATTTCTCTCAAGAGATCC 3230

RESULT 2  
 US-09-755-633-18  
 ; Sequence 18, Application US/09755633  
 ; Patent No. US20020127200A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: McCall, Catherine A.  
 ; APPLICANT: Weber, Eric R.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; FILE REFERENCE: IM-2-C1-C1  
 ; CURRENT APPLICATION NUMBER: US/09/755, 633  
 ; CURRENT FILING DATE: 2001-01-05  
 ; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087,306  
 ; PRIOR FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: Patent Ver. 2.1  
 ; SEQ ID NO 18  
 ; LENGTH: 1658  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 ; FEATURE:  
 ; NAME/KEY: Intron  
 ; LOCATION: (171)..(373)  
 ; NAME/KEY: Intron  
 ; LOCATION: (407)..(1275)  
 ; NAME/KEY: Intron  
 ; LOCATION: (1405)..(1522)  
 US-09-755-633-18

Query Match 18.6%; Score 600.6; DB 10; Length 1658;  
 Best Local Similarity 67.8%; Pred. No. 3.2e-109;  
 Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;

Oy 527 AGGCAAGCGAGAGGTTTCAAGGACATGAGATGCTTTCATTTGAGTTTGGTACTG 586  
 Db 1 AGGCAAGCGAGAGGTTTCAAGGACATGAGATGCTTTCATTTGAGTTTGGTACTG 60  
 Oy 587 TTGAGAGCTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 646  
 Db 61 TTGAGAGCTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120  
 Oy 647 AGAGCTTGGACCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 706  
 Db 121 AGAGCTTGGACCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 Oy 707 TTATGATTTCTGACAGTCTGTAAGGATGATGATGATGATGATGATGATGATGATGATGAT 766  
 Db 181 TTATGATTTCTGACAGTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 234  
 Oy 767 ATATAGAGATCTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 825  
 Db 235 -TTTAAAGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 293  
 Oy 826 ACATACACAGCAAACTTCTGTTAAAGTTATGATGATGATGATGATGATGATGATGATGATG 885  
 Db 294 ATGTTACACAGCAAACTTCTGTTAAAGTTATGATGATGATGATGATGATGATGATGATGATG 353  
 Oy 886 -TATTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944  
 Db 354 TTGTTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 413  
 Oy 945 AAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1004  
 Db 414 AAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 469  
 Oy 1005 TCATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1064  
 Db 470 GTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 529  
 Oy 1065 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1109  
 Db 530 AAAT-TATGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 588  
 Oy 1110 GAATCCTTTAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1169  
 Db 589 GAATCCTTTAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 648  
 Oy 1170 AGATCGTGTAGG-ATCTTCTTCAAGAGATTTCCACACTAGAGAGAGGCTGCTGCTAG 1228  
 Db 649 ACCCTCGTGTAGGAGATTTCTTCAAGAGATTTCCACACTAGAGAGAGGCTGCTGCTAG 708  
 Oy 1229 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1283  
 Db 709 GCTCATTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768

QY	1284	ACGAGATTTATTTTTTAGACACGATGAGTAGACATTAATAATATACAAATGCC-	1342
Db	769	ACTTGGGGTATATTTTTTAGATTATGTGATGACATGAAAATATACAGTAAGCTCT	828
QY	1343	--CATATTAATTAATCTGCATACCTGTAATAATTAAGCTATATGATGTGTATGCAT	1400
Db	829	ATATTAATAGTACCTTCACATATTTTAATGATTTTTTAOCTTAATGCAATCATATACAT	888
QY	1401	TGAATAT---GCTGGTCAATTTTAAATGTAAATATAT-AGTTATATGTCTAAATGGA	1456
Db	889	CTGAGATGTCAAGGTCATATTAATTAATGATATCATATGCTGCTAAATAGA	948
QY	1457	ATTAACACTACAGCTAGACACTGTAGAAACACAT--TGATATAGTTAATGTATATATGC-	1513
Db	949	ATTAATATTCACAGCTAGACATATTCGAGGAATTTCTGAGGTGAGGTAAATCTAGTAAGCA	1008
QY	1514	----ATTACACTTCCAAAACATTTTTTTCAGTACATATTAATTAAGTATATCTTTATA	1568
Db	1009	GTTGATATTAATACCTGTACACATATTTATTTTTCATTAATCATTTTATATCATTTGTA	1068
QY	1569	AAACCCCACTATTCATTAATTAAGCTCATCTACTTTTGAAATTTTATCTTAATATGTG	1628
Db	1069	ACACTTTCATATTAATTAATTAACATCATTTAC--TTATGTATTAATTAACCTTAGTATAG	1127
QY	1629	GTTGGTTGTTCCCTAGAGAA---ACAAACAAAACCTCTTTGAGAGGAAGCATATGTA	1684
Db	1128	GTTGGTTCCACCTGTGAAAAGACACAAAGTAAAACTCTTGGAGAGAGAACTGTGTATA	1187
QY	1685	AATACACAAAACAAAGCCTTAACCTTTGTGGACCCAAAATGTTTTTAATTAATTTTTTAA	1744
Db	1188	AAACCCCAAAAACAAAGCTCTACACCTTTT-----	1214
QY	1745	TTGATGATTTAAAGATATATATTTATTTGTGTACAAATATATGTTTGAAGTATGAT	1804
Db	1215	-----	1214
QY	1805	ACATTTGAGAAATGCAATGAGAACAAATTTTTATACCTTGTCTTGATTAATTTGCA--TTTT	1863
Db	1215	-----TGACCAATTTTTTATGCTTTGTGATGATATATTTTTT	1256
QY	1864	AAAAATTTTCTCATTTTAGACACCAACTGTGTACACTGTAGAAATCTTTACAGCAATATGCGAC	1923
Db	1257	TAAATATCTCTCTCTTTTATGACCAACACTGTGCATTAAGTAAGGTTTTACAGGGATATAGACAC	1316
QY	1924	ACTGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAACATTAATCAAAAACCTGTCTT	1983
Db	1317	ATTGAGAGACCAAACTGCCACAGGGAGGCTGTGGGATAACTATTTCCAAAACCTGTCTTT	1376
QY	1984	AATTAAGAAATATACATTTGACGGCCAAAAGATAGATTACACATTCATATGAGAACTATAT	2043
Db	1377	AATTAAGAAACACATATAGAGGCCCCAAAAGTAAGTTAAAGCATTTGGCAAAAACCTTAAGT	1436
QY	2044	TGTCCTGGCTG-----TGCCATATTTCTATGCAATTTGACAGTTTCTGTG	2085
Db	1437	ATATTTGTCTGACTCTGCTGTTTTTTTTTTTTTTTTTTTATACAAAGTAATGACAGTTTCTTA	1496
QY	2086	TAAATACCTATTTGCATTTTTTTCTTTTTCACAGAAAAGTGTGAGAAAGAAAGACGAGAG	2145
Db	1497	CATATATCT-----CCTGTGTTCTTTTAAACAGAAAAGGTGTGCAGAGAAAAGATGAGAG	1550
QY	2146	TAAACCAATTTCTTAGACTATCTGACGAAGATTTCTTGTTGTGTAATGAAACGAGTGTGATTA	2205
Db	1551	TGACAAAGTTCTTAGACTATCTGCAAGATTTCTTGTTGTGTAATTAACACCGAGTGTGACAC	1610
QY	2206	TAGAAAGTTGAGACTAAACGTGTTGTGTGTGACGCAAAAAGTTTTTGGAG	2252
Db	1611	CGGAAAGTTGAGACAAACCGGCTTATTTGTAGTGGAGAAAGTTTTTGGAG	1657

Patent No. US20020127200A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/09/755,633  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-25  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 1658  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-755-633-19

Query Match	18.3%	Score 589.6	DB 10	Length 1658
Best Local Similarity	67.4%	Pred. No. 4.8e-107		
Matches 1206	Conservative 0	Mismatches 389	Indels 193	Gaps 19
QY 527	AGGCAACGCAACGACGTTTCAGAGCCATGAGAGATGCTCTTCGACATTTGAGTTGCTCTAGCTC	586		
Db 1658	AGGCAACGCAACGACATTTTCAGAGCATATGACAAATGCTCTCGAATTTGAGTTGCTCTAGCTC	1599		
QY 587	TTTGAGGTGCTTACGCTGATGCCATCCCCACAGAAATTTCCACAGATGCAATTGGTGAAAG	646		
Db 1598	TTGGGGGTGCTATGTTTCTGCTTGGCTGTAAGAAATCCCATMAATAGCATGCTGGGCGAG	1539		
QY 647	AGACCTTGGACGCTCTTCTACTACATCGACACTGCTGCTATGAGCCATGAGGATTAATTTCT	706		
Db 1538	AGACCTTGGACGCTCTCTCTCACTCATCTCGAATCTGGCTGATAGCGGATGGGATATTTTCT	1479		
QY 707	TTATGATTCCTACAGTCTGTAAAGTGACATGATTAATCTTTGTGATGATGCTCTTACTAT	766		
Db 1478	TTTGTGATTCCTACAGTCTTTAAATATGACATGGGATATGGTGCTGCTAGTT-----	1425		
QY 767	ATATAGGATCTGTATTAATTAATTAAGATTCGA--GCACATTATGATACAGGCTGATAC	824		
Db 1424	TTTAAAGATCCATTTCAATTAATTAATTAATGATGATTAATTAATTAATTAATTAATGAGGTAC	1366		
QY 825	TACATCACGACGCAACATCTGTAAAGTATTAATGATAGCTGGGTGCTGTAATAAATGAT	884		
Db 1365	CAGTTCATCTCAGAGAGATTAATTAATAAGTTATGACCTTATCAATTAATTAATAAATGAAT	1306		
QY 885	G-TATTTCTCTTCTCTCCAGACTGTGAGATTCCTGCTCTCTGTCATTAATAATGTAGT	943		
Db 1305	GTTGTTTCTCTCTTTTTCAGAACTGATGATTCCTCTCTGTAATAAATAATGTAGT	1246		
QY 944	TAAATATGATTCAGTAAATATGTCGCATGAATTAAGTAATAATTCCTGTTTAACTGTAA	1003		
Db 1245	TAAATATGATTTGTAATAAATGATTCATGATGATGAG---TTTCATATTTTAACTGTAA	1190		
QY 1004	ATCATTTGATTAATCGAATCATTTAATTTTCAATATTTTGTTCATATAGGTCGGCG	1063		
Db 1189	AGATTCAGTTTAACATTTGGGATGATTTAATTTTATTCATATTTTGTGTTTATGTCGGGAG	1130		
QY 1064	TGAATGCTGTACTATAAATATGAGGATGACTT-----TTATCAAGT	1108		
Db 1129	TATAT-TATGTGCTTATGAAATATTTGAAATGCTGTGAGGATGGCTCTCAATATTAAGT	1071		
QY 1109	AGAACTCTTAAACAAGTGGATTAAGCTCTTTGGTATGTTTGAATTTGCTTCCCAAA	1168		
Db 1070	AGATTCATTAAGCAAGTGGATGAGGCTCTTTTGTGATTTGTCAGTCTCCATCCAAA	1011		
QY 1169	GACATCTGTGTGAGG-ATTCCTTCAGAAAGATTCACACATGATGAGGAGGTCGCTGA	1227		
Db 1010	GACCTCTGTGTGAGGATTTTCCAAAAGATTCATATTTGGTCTGAGATTAATCTTCA	951		

OY	1228	GTCTCCCTGAGAGTCTGAC-----CTCTTCTCACTCTACAGTGGTTTCTGAAAGTTTGGC	1282
Db	950	GGCTCCACTTCACTCTCTCTGCTTGGCTTCTCTCACTCACTCAACGTTTTTCTGAAAGTACTAGC	891
OY	1283	AACTCAGAAATTATATATTTTGAACCATGATCACTAGACATTTAAATATATACAACATGCC	1342
Db	890	AACCTTGGGGTATATATTTTGAATATATGTCAGCTAGACATGAAATATACAGTGAAGTCC	831
OY	1343	---CTATATTAATATATCTGCACTACTAAATAATATGACTATATGATNGTGTGTATGCA	1399
Db	830	TATATATATATAGTCACTTCCACATATTTAAATGATTTTAACTCTAATGCAATCATATCA	771
OY	1400	TTGAATAT--GCCGTGCTATATTTAAATATGTAATAATATAT-AGTTTATATGCTAAATAG	1455
Db	770	TCTGAGATAGTCAATGGTCAATTTAAATAGTTAAATGTAATGATATCATATAGCTAAATAG	711
OY	1456	AATTAACCTACACAGCTAGAACCTGTAACAAACACT--TGATATGACTTTATGTTATATATGC	1513
Db	710	AATTAATTTACACAGCTAGAACCTATACGAGAAATTTCTGAGGTAGAGTAAATACAGTAGGC	651
OY	1514	-----ATTACACTCCAAACATTTTTTTTCCAGTACATATTAAGTATATCTTTAT	1567
Db	650	AGTTGATATATACCTGCTAGGCAATTTATTTTTCATTAATCATTTCTATATATATTCATTGGT	591
OY	1568	AAAACCTCCTGATATCATATTAAGCTTCATCTATTTTTGAAATTTTATCTTAAATATGT	1627
Db	590	AACACTTCTCAGTATATATATTAACATCATTTAC--TTATGTAATATATAGCTTACTATATA	532
OY	1628	GGTGGTTTGGTGGCTACAAA-----ACAAACAAAACCTGTGGAGAAAGGAAACATCATGT	1683
Db	531	GGTGGTTTCCACCCTGGGAAAGACAGATTAATAAACCTCTGGGAGAAAGGAACCTTGGT	472
OY	1684	AAATACACAAACAAAGCCCTAACTTTGTGGACCAAAATGTTTTAATATATTTTTTTTA	1743
Db	471	AAACCCACAAACAAAGCTAACTTT-----	445
OY	1744	ATTATGATATTTAAAGATATATATATTTATTTGTTACAAATATGATGTTTTGAAATATGTA	1803
Db	444	-----	445
OY	1804	TACATTCGAGATATGGAACAATGAGACCAAAATTTTATATACCTGTGCTTGATTAATTTGCA--TTT	1862
Db	444	-----TGACCAAAATTTTATGCTCTTTGTTCATATATATATTTT	404
OY	1863	TAAAAATTTTCTCATTTAGTACCAACAATGTCACGTAAGAANAATCTTTCAGGGAATAGGCA	1922
Db	403	TTAAATATCTTCTCATTTTACCAACAATGTCATTTAAAGAAAGTTTTTTCAGGGTATAGACA	344
OY	1923	CACGTGAGAGTCAACATGTCGAAGGGGGTACGTGTGAAAGACATATTCACAAAACCTGTCT	1987
Db	343	CATTGAAGAACCAACATGTCACGAGGGAGGCTGTGATTAACATATTCACAAAACCTGTCT	284
OY	1983	TAAATTAAGAAATATACATTTGACGGCCAAAAAAGTAAGTTATACACATCTCAATGAAGCACTATAT	2042
Db	283	TAAATTAAGAAACACATATGAGCGCCAAAAAAGTAAGTTAAAGACATTTGGCAAAAACCTTAAG	224
OY	2043	TTGTCTTGGCTG-----TGCCATTTCTATGACATTTGACAGTTTCT	2088
Db	223	TATATTTGTCTGACTGCTCGTTTATTTTTTTTTTTTTTTTATACAAAGATTTGACAGTTTCT	164
OY	2085	GTAATACCTATTTGTCATTTTTTCTTTTTTTCACAGAAAAGGTGGAGAACAAAGACGGGACA	2144
Db	163	ACATATAT-----CCTGTCTTTTAAACAGAAAAGGTGTGACGAGAAAGATGAGGA	110
OY	2145	GTAACCAATTTCTAGACTACATCTGCAAGAAGTTCTTGTGTAAATGAACACGAGTGGATA	2204
Db	109	GTCAGAAAAGTCTTAGACTACCTGCAAGTATTTCTTGCTATATTAACACCAAGTGGACA	50
OY	2205	ATAGAAAATGTAGACTAAACATGGGTTTTTGTACAGCAAAAGTTTTTGGAG	2252
Db	49	CCGGAAGTGTAGAACAAACCGGCTTATTTGTAGTGAAGATTTTTTGGAG	2

RESULT 4  
 US-09-755-633--21  
 : Sequence 21, Application US/09755633  
 : Patent No. US20020127200A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Yang, Shumin  
 : APPLICANT: McCall, Catherine A.  
 : APPLICANT: Weber, Eric R.  
 : TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 : TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 : FILE REFERENCE: IM-2-C1-C1  
 : CURRENT APPLICATION NUMBER: US/09/755,633  
 : CURRENT FILING DATE: 2001-01-05  
 : PRIOR APPLICATION NUMBER: 09/332,409  
 : PRIOR FILING DATE: 1999-05-28  
 : PRIOR APPLICATION NUMBER: 60/087,306  
 : PRIOR FILING DATE: 1998-05-29  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 21  
 : LENGTH: 671  
 : TYPE: DNA  
 : ORGANISM: Canis familiaris  
 US-09-755-633--21

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Query Match Summary      6.3%; Score 205; DB 10; Length 671;
Best Local Similarity   73.6%; Pred. No. 3,76-31;
Matches    304; Conservative    0; Mismatches 100; Indels    9; Gaps    3;

OY  527 AGGCAACGCAGAACGGTTTCAGAGCCATAGAGANTCCTTCTCGCATTTGAGTTTGCTAGCTC 586
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   1  AGGCCAACAAGTGAACATTTCAGAGGTATAGAGATGCTTCTGATTTGATTGGTAGCTAGCTC 60
OY  587 TTGGAGCGTCTAGCTGTATGCCATCCCACAGAATAATCCCAAGAATGCATTTGGTGAAG 646
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   61 TTGGGGCTGCTCTATSTTTTCTGCTTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAG 120
OY  647 AGACCTTGGCACCTGCTTTCTACTCATCGAACTCTGCTGATAGCCAATGAGTAATTTTCT 706
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   121 AGACCTTGACACTGCTCTCCACTCATCCAACTTGGCTGATAGGCGATGGGTAATTTTCT 180
OY  707 TTATGATTCCTCAACTCTGCTGAAGCGCATAGTATCATTTGTATGCTTCTTACTAT 766
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   181 TTTTATTTCTCAACAGCTTTTAAAAAGCATGGGTATTTGTTGGTGGCTGATT----- 234
OY  767 ATATAGAGATCTGTTATATAATATATAGATTTCGAG-CACATTAGTACATGGGTGATTA 825
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   235 -TTTAAAGTCATTTATCAATATATGAAGTAATGAATGTTAATATATATATATGTTGTTAAC 293
OY  826 ACATCACACGCAACATTTCTGTTAAAGTTATGAATGCTGCTGCTGTAAAAATGATGTT 885
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   294 ATGTACTCCAGAAAGATTATATATAAGTTTAAAGCTTACAAATCATTTAAAAATGAATG 353
OY  886 -TATTTCCCTTCCCTCCAGACTCGAGAGATCCGTTGCTCTGATACATTAAT 937
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   354 TTGTTTCCCTTTCTTTTCAGAACCTGATGATTTCTACTCTCTGAAAAATTAATAAT 406

RESULT 5
US-09-800-629A-1
Sequence 1, Application US/09800629A
Patent No. US20020128216A1
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G
APPLICANT: McKay, Robert
APPLICANT: Manoharan, Muthiah
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
FILE REFERENCE: ISPH-0537
CURRENT APPLICATION NUMBER: US/09/800,629A
CURRENT FILING DATE: 2001-03-07

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Query Match	3.1%;	Score 99.4;	DB 10;	Length 402;
Best Local Similarity	75.28;	Pred. No. 2.3e-10;		
Matches 124; Conservative	0;	Mismatches 41;	Indels 0;	Gaps 0.

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; FILE REFERENCE: 1M-2-C1-C1
;
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28

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;; PRIOR APPLICATION NUMBER: 60/087,306  
;; PRIOR FILING DATE: 1998-05-29  
;; NUMBER OF SEQ ID NOS: 21  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 345  
;; TYPE: DNA  
;; ORGANISM: Canis familiaris  
US-09-755-633-11

Query Match 2.8%; Score 90.2; DB 10; Length 345;  
Best Local Similarity 76.9%; Pred. No. 1.4e-08;  
Matches 110; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1881 AGCAACACTGTGCACATGAAGAATCTTCAGGAGTAAGCAGACATGAGAGTCAACTG 1940  
DB 227 ATACCAACTGTGCATTAAGAAGTTTTCAGGTTATAGACACATTTGAAGAACCAACTG 168  
QY 1941 TGCAGGGGGTACTGTGGAAGACTATTCAAAACTTGCTTAATTAAGAATACATTG 2000  
DB 167 CCCACGGGGAGCTGTGATTAACCTATCCAAACTGCTTAAATTAAGAAGACACATAG 108  
QY 2001 ACGGCCAAAAAGTAAGTTACACA 2023  
DB 107 AGCGCCAAAAAGGTGTGCA 85

RESULT 12  
US-10-092-154-1550  
;; Sequence 1550, Application US/10092154  
;; Publication No. US20030054375A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC009C1  
;; CURRENT APPLICATION NUMBER: US/10/092,154  
;; CURRENT FILING DATE: 2002-03-07  
;; NUMBER OF SEQ ID NOS: 2003  
;; Prior Application removed - See File Wrapper or Palm  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 1550  
;; LENGTH: 32187  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-092-154-1550

Query Match 1.9%; Score 61; DB 9; Length 32187;  
Best Local Similarity 61.8%; Pred. No. 0.066;  
Matches 97; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1706 ACTTTGTGACCAAAATGTTTAATTAATTTTAAATGATGAATTAAGATATAT 1765  
DB 9369 ACTTTCTAATACACGACGAGCTTTGTTTATTAATTAAGCTGACAAATAAATTTGAT 9428  
QY 1766 ATATTATTTGTGACAAATGATGTTTGAAGATGATACATTCAGAAATGACAAATG 1825  
DB 9429 ATATTATTTGTGACAAATGATGTTTGAATGATACATTCAGTGGAAATGTTTAA 9488  
QY 1826 ACCAAATTTTATACCTGCTGTGATTAATTTGCAATT 1862  
DB 9489 GCTAATTAGCATTAACATACATTAACCTTTTTT 9525

RESULT 13  
US-09-764-847-1550  
;; Sequence 1550, Application US/09764847  
;; Patent No. US20020132767A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC009  
;; CURRENT APPLICATION NUMBER: US/09/764,847  
;; CURRENT FILING DATE: 2001-01-17

;; Prior application data removed - consult PALM or file wrapper  
;; NUMBER OF SEQ ID NOS: 2003  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 1550  
;; LENGTH: 32187  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-764-847-1550

Query Match 1.9%; Score 61; DB 10; Length 32187;  
Best Local Similarity 61.8%; Pred. No. 0.066;  
Matches 97; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1706 ACTTTGTGACCAAAATGTTTAATTAATTTTAAATGATGAATTAAGATATAT 1765  
DB 9369 ACTTTCTAATACACGACGAGCTTTGTTTATTAATTAAGCTGACAAATAAATTTGAT 9428  
QY 1766 ATATTATTTGTGACAAATGATGTTTGAAGATGATACATTCAGAAATGACAAATG 1825  
DB 9429 ATATTATTTGTGACAAATGATGTTTGAATGATACATTCAGTGGAAATGTTTAA 9488  
QY 1826 ACCAAATTTTATACCTGCTGTGATTAATTTGCAATT 1862  
DB 9489 GCTAATTAGCATTAACATACATTAACCTTTTTT 9525

RESULT 14  
US-10-092-154-1549  
;; Sequence 1549, Application US/10092154  
;; Publication No. US20030054375A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC009C1  
;; CURRENT APPLICATION NUMBER: US/10/092,154  
;; CURRENT FILING DATE: 2002-03-07  
;; NUMBER OF SEQ ID NOS: 2003  
;; Prior Application removed - See File Wrapper or Palm  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 1549  
;; LENGTH: 32193  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-092-154-1549

Query Match 1.9%; Score 61; DB 9; Length 32193;  
Best Local Similarity 61.8%; Pred. No. 0.066;  
Matches 97; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1706 ACTTTGTGACCAAAATGTTTAATTAATTTTAAATGATGAATTAAGATATAT 1765  
DB 9368 ACTTTCTAATACACGACGAGCTTTGTTTATTAATTAAGCTGACAAATAAATTTGAT 9427  
QY 1766 ATATTATTTGTGACAAATGATGTTTGAAGATGATACATTCAGAAATGACAAATG 1825  
DB 9428 ATATTATTTGTGACAAATGATGTTTGAATGATACATTCAGTGGAAATGTTTAA 9487  
QY 1826 ACCAAATTTTATACCTGCTGTGATTAATTTGCAATT 1862  
DB 9488 GCTAATTAGCATTAACATACATTAACCTTTTTT 9524

RESULT 15  
US-09-764-847-1549  
;; Sequence 1549, Application US/09764847  
;; Patent No. US20020132767A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC009  
;; CURRENT APPLICATION NUMBER: US/09/764,847  
;; CURRENT FILING DATE: 2001-01-17  
;; Prior application data removed - consult PALM or file wrapper



